

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:32:55 : Search time 3720.62 Seconds
(without alignments)
11745.631 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 0
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : GenEmbl.*

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
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- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_om.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
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- 25: em_ro.*
- 26: em_sts.*
- 27: em_sy.*
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- 32: em_htgo_rod.*
- 33: em_htg_hum.*
- 34: em_htg_inv.*
- 35: em_htg_rod.*
- 36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2547	96.1	2650	8	PSU67185	U67185 Papaver som
2	29	1.1	2493	8	AF302497	AF302497 Hybrid po
3	26	1.0	2114	6	A75959	A75959 Sequence 1
4	26	1.0	2199	8	ATATRI6	X66016 A.thaliana
5	26	1.0	2498	8	AF302496	AF302496 Hybrid po
6	26	1.0	125803	8	ATF22K18	AL035356 Arabidops
7	26	1.0	198402	8	ATCHRIV61	AL161561 Arabidops
8	24	0.9	2641	8	VSNER	Z26252 V.sativa mr
9	24	0.9	129332	9	AL590028	AL590028 Human DNA
10	24	0.9	161486	2	AL590008	AL590008 Homo sapi
11	24	0.9	163603	2	AC026755	AC026755 Homo sapi
12	23	0.9	1864	10	BC011090	BC011090 Mus muscu
13	23	0.9	2466	8	AF024634	AF024634 Petroseli
14	23	0.9	2545	8	AF002698	AF002698 Pisum sat
15	23	0.9	2617	8	VIRNADPH4	L07843 Vigna radi
16	23	0.9	2631	8	PM14CPR	Z49767 Pseudotsuga
17	23	0.9	160708	2	AC068406	AC068406 Homo sapi
18	22	0.8	1821	8	AB007405	AB007405 Oryza sat
19	22	0.8	2385	8	AF130425	AF130425 Lycopersi
20	22	0.8	2556	8	AF024635	AF024635 Petroseli
21	22	0.8	17643	8	AC079287	AC079287 Arabidops
22	22	0.8	65262	2	AC025908	AC025908 Arabidops
23	22	0.8	75133	8	F2H15	AC034106 Sequence
24	22	0.8	77040	8	AC004484	AC004484 Arabidops
25	22	0.8	87967	8	AC005223	AC005223 Arabidops
26	22	0.8	199421	2	AC051636	AC051636 Homo sapi
27	21	0.8	235	5	MGU79352	U79352 Meleagris g
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29	21	0.8	425	3	PFU72623	U72623 Plasmodium
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ALIGNMENTS

RESULT 1	PSU67185	2650 bp	mrna	PLN	06-MAR-1998
LOCUS	Papaver somniferum	NADPH:ferrihemoprotein oxidoreductase mrna,			
DEFINITION	complete cds.				
ACCESSION	U67185				
VERSION	U67185.1	GI:2580496			
KEYWORDS					
SOURCE	Opium poppy.				
ORGANISM	Papaver somniferum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales; Papaveraceae; Papaver.				
AUTHORS	1 (bases 1 to 2650)				
TITLE	Rosco.A., Pauli.H.H., Priesner,W. and Kutchan,T.M.				
JOURNAL	Cloning and heterologous expression of NADPH-cytochrome P450 reductases from the Papaveraceae				
MEDLINE	Arch. Biochem. Biophys. 348 (2), 369-377 (1997)				
REFERENCE	98096363				
	2 (bases 1 to 2650)				

AUTHORS Rosco,A. and Kutchan,T.M.
TITLE Direct Submission
JOURNAL Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,
Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany
FEATURES Location/Qualifiers
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124. .2175
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reduces cytochrome c"
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Matches 2647; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1561


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REFERENCE 1 (bases 1 to 2114)
AUTHORS Kazmaier, M. and Lacroute, F.
TITLE METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
JOURNAL NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES
PATENT: WO 9321326-A 1 28-OCT-1993;
ORSAN (FR); KAZMAIER MICHAEL (FR)
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Qy 1954 tatgttcaacataagatgatgagaa 1979
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Db 1893 TATGTTCAACATAAGATGATGGAGAA 1918

RESULT 4
LOCUS ATATRIG 2199 bp mRNA PLN 01-JUN-1992
DEFINITION A.thaliana ATRI mRNA for NADPH-cytochrome P450 reductase.
ACCESSION X66016.1
VERSION x66016.1 GI:16186
KEYWORDS ATRI gene; NADPH-ferrihemoprotein reductase.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2199)
Pompon, D.M.
Direct Submission
Submitted (11-MAY-1992) D.M. Pompon, Centre de Genetique Mol du
CNRS, Avenue de la Terrasse, 91198 Gif-Sur-Yvette Cedex, FRANCE
2 (bases 1 to 2199)
Mignote-Vieux, C., Kazmaier, M., Lacroute, F. and Pompon, D.M.
Unpublished
Location/Qualifiers
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REFERENCE 1 (bases 1 to 2114)
AUTHORS Kazmaier, M. and Lacroute, F.
TITLE METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
JOURNAL NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES
PATENT: WO 9321326-A 1 28-OCT-1993;
ORSAN (FR); KAZMAIER MICHAEL (FR)
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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1893 TATGTTCAACATAAGATGATGGAGAA 1918

RESULT 5
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DEFINITION Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome
P450 oxydoreductase isoform 1 mRNA, complete cds.
ACCESSION AF302496
VERSION AF302496.1 GI:13183561
KEYWORDS
SOURCE
ORGANISM Populus x generosa.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Malpighiales; Salicaceae; Populus.
1 (bases 1 to 2498)
Ro, D.-K. and Douglas, C.
Functional characterization of cytochrome P450 reductase from the
hybrid poplar (Populus trichocarpa X P. deltoides)
Unpublished
2 (bases 1 to 2498)
Ro, D.-K. and Douglas, C.
Direct Submission
Submitted (05-SEP-2000) Botany, University of British Columbia,
6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada
Location/Qualifiers
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        84..2162
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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1946 aagaggaatatttcacataaagatg 1971
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Db 1933 AGAAGGAATATGTCACATAAAGATG 1958

RESULT 6
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LOCUS
DEFINITION Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII
project).
VERSION AL035356
KEYWORDS AL035356.1 GI:4220510
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 125803)
Bevan, M., Wedler, H., Wedler, E., Wambutt, R., Hoheisel, J.,
Mewes, H.W., Mayer, K.F.X. and Schueller, C.
Unpublished
2 (bases 1 to 125803)
EU Arabidopsis sequencing, project.
Direct Submission
Submitted (03-FEB-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
schueller@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosome 4 can be
viewed at: http://weber.mips.biochem.mpg.de/proj/thal/.
FEATURES
source
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/variety="Columbia"
/db_xref="taxon:3702"
/chromosome="4"
171..2980
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1556..2980))
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/number=1
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1556..2980))
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CDS
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1556..2980))
/gene="F22K18.10"

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/note="similarity to DNA polymerase III gamma subunit -
Aquifex aeolicus, PIR2:A70460
Contains ATP/GTP-binding site motif A (P-loop) [GPRGTGKT]"
/codon_start=1
/product="DNA polymerase III like protein"
/protein_id="CAA22984.1"
/db_xref="GI:4220511"
/translation="MGETRRHSVDVPIITLVALRRVRSURDPCCTTSMKSFASLLDNY
KWTGNGNIGISQFVHADDAKAAADAPVGLIPFGSYSIMEELESGCDLHKLSKVI
NVGDGACSSRSRCSDLVKGRDLACNAPISHVBEAGSGGRYRTHYSTPKLASSVGE
YSGRLGSPMNSTNHSYVGDVDVDFDSQNRGCGITYCWSRTPRYGRSNQSSDVEEYPL
LPNGGSGDVYTPSHSVLSRLSQFRPKSFDLVCQEVVVKCLLSTILGRITSVY
LFHGPGRGTSTSKFAAALNCLSQAAHSRPGCLCECKSYFSGRGRDVMETDQKGL
NRPSYLSLTKSASLPVSRFRKFIIDECQLLCOETGWTLLNSLDFNSQHSVFILVT
SELEKLPNRVLSRSQKYHFSKQCDADISTKLAKICIEGIDFQDQAVDFTASKDQSL
RDAEIMDQLSLGKRITTSYLAVKLVGVSDDELDDLAMSDDTNTVIRARELMR
SKIDPMQLISOLANIMDIAGNSQESSSATRLRTRHTSEEMOKLRNALKILSDA
EKHLRASKNOTTHLTVALQLQSLNTDSSSATDENGQINKDVELSTSGCGFGDVIK
SDAEKGOERNCTNETSVWKTVDLCCSDSLKRFUWRGRRLTSLTVKGVAVIAELFAY
TPQHVARAKSKMLIADSFQVLCNVEIQMLNLIISACSPPKAKAAASLFFGLFSCS
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PATX:E209876"
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GPCITIQYVTNIIIGHIHIDCKQGNAMVRSRPHFWRTISDGDGVSIFGGSHVWV
DHCFSNCEGDLIDMGSTAITLSNNHTIHDKVMLLGLHSDTYSRDKNNQVTFIAFNH
FGELGVQRMPRHGYFHVWVNDYTHWEMYAIGGSANPTINSQGNRFLAPNTRFSEVTK
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/number=2
10120..10216
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 /note="cp31 is 100% homologous but lacks a 15 AS stretch
 in the first exon, position 106 to 120
 Ribonucleoprotein
 Contains Eukaryotic putative RNA-binding region RNP-1
 signature [RGFGFTVM], [RGFGFTVM]
 contains EST gb:AA395600, A1100105, T45260, T76407,
 T43174, R90420, T22781, H76412, R64751, T21054, T20937,
 N96937, AA713138"
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 VNSQAAMLEFEQAGTVEIAEVYINRETDQSGFGFTVMSSVDEAETAVEKFNVDLNG
 RLITVKAAPRGSRPERAPRVPAFRVYVGNLFDVDNGRLQLFSEHGKVVVEARVY
 YDRETRGSRGFGFTVMSVDDELNEAISALDQNLGRAIRVNVAAERPPRRGY"
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 Arabidopsis thaliana, PATX:E1283548"
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 PRRLASILHSPILSLGRLVMPVKRTYWFIDYIKNIDITLVRCPLVHIGTFADVDVDF
 HGKQLNELCOKEPLWLGKGNHCDLELPEYIGHLKKFVSAVEKSAKRNKNSFSRRS
 MECCEQPPHRSVDAPKSKDGRKPKRSIDRLRFQYKLSHIEKPKLKVPFEMERS
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 17940. .18590
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 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1954 tatgttcaacataagatgatggagaa 1979
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 Db 117747 TATGTTCAACATAAGATGATGGAGAA 117772
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 RESULT 7
 ATCHRIV61/c
 LOCUS ATCHRIV61 198402 bp DNA PLN 16-MAR-2000
 DEFINITION Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61.
 ACCESSION AL161561
 VERSION AL161561.2 GI:7269265
 KEYWORDS
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 (bases 4709 to 5139)
 AUTHORS Robben,J., Grymonprez,B., Volckaert,G., Mewes,H.W., Lemcke,K. and
 Mayer,K.F.X.
 JOURNAL Unpublished
 REFERENCE 2 (bases 16658 to 125116)
 AUTHORS Zimmermann,W., Grueneisen,A., Wambutt,R., Kalicki,J., Wohldmann,P.,
 Smith,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
 JOURNAL Unpublished
 REFERENCE 3 (bases 123107 to 198402)
 AUTHORS Wedler,H., Wedler,E., Wambutt,R., Mewes,H.W., Lemcke,K. and
 Mayer,K.F.X.
 JOURNAL Unpublished
 REFERENCE 4 (bases 1 to 20862)
 AUTHORS Peters,S.A., van Staveren,M., Dirkse,W., Stiekema,W., Mewes,H.W.,
 Lemcke,K. and Mayer,K.F.X.
 JOURNAL Unpublished
 REFERENCE 5 (bases 1 to 198402)
 AUTHORS EU Arabidopsis sequencing,project.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
 Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
 E-mail: michael.bevan@bbsrc.ac.uk
 COMMENT Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
 this fragment has an overlap with ATCHRIV60 at the 5' end and an
 overlap with ATCHRIV62 at the 3' end.
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 exon
 gene

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8876..9036,9206..9315,9402..9501,9574..9697,9790..9918)
/gene="At4g24160"
/notes="similarity to CGI-58 protein - Homo sapiens,
PID:g4929585
Contains prokaryotic membrane lipoprotein lipid attachment
site AA376-386
contains EST gb:AI099669, T21097, AA394561, T76500,
T42730"
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RWLPTSDYIIAAEKRLLSILKTPYVOEQVSGGPPGSKIRWRSTSNESRYINTVT
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ETAEWFDSFEENRKAQNLNFIILLHSGFGYVAAKYALKHPHVQHLLILVGSAGRSA
EADAKSMLVFRATNRGAVLNHLWSENFTPQKLVRLGLGHPWGLVNRVYITARFGAHS
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12026..12213
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CDS
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14692..14793,14875..15081,15183..15231,15323..15374,
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/gene="At4g24170"
/notes="similarity to kinesis heavy chain
-Strongylocentrotus purpuratus, PID:g10270
Contains ATP/GTP-binding site motif A (P-loop)
AA89-96:Kinesin motor domain signature and profile
AA225-236"
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PDKSSTDFKVFGEFECTKQVYDDGAKVEALCVLSGINSISIFAYGQTSSGKTYTMSGI
TEFAMDDIFAYIDKHQERKFTLKFSAMEIYNEAVROLLCEDSTPRLRDDPGRGIV
VEKLRETLDRSHLELLSICETQKIGETSLNEISSRSHQILRLTIESSQQFSPE
SSATLAASVCFVDLAGSERASQTLASGRLEKGCCHINRSLTLGTIVRKLSKGNKGI
PYRDSKTRILQNSLGSNARTAICTWSPARSHLEQSRNTLLPATCAKEVTTNAQVNL
VVSEKALVKOLORELAEMENELKNGPASASSTDYFALMLKKEELIAKMEEOIHLEL
KWORDVAQSRVENLLKSTABERSSSSSMDSRRRRIISYDSTDFDEPRMLNLGKSNLIS
PDEDGLDLDTTQFPGHNLHDKWEEMAQSTQEPDACKREVCIEVNSGEAEKRVIQ
DSLDDIIVEKKEYEONYESQKDDADSSIKNIDMELSLYTKPEADGVSVKKLIEDVQET
EQSVYKQKQSPKKEEMEQYLSRDMSEQVTKSLPEEQCVQVEYDAYDKLEAQDVLTIK
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FLLFKGPDSDFVYNEVELRSLFLKSTETSRKOTAKAVTREREMLAQIQPNKFGKKE
KEEYKKGWVGLSSKRRSLQVTKHLNNNTKDIHCKESASLIATLVGFVDSLTLPKE
ISDLGTLPELMAQLIRPIQLSPQCNHFRNLSPRRIRPAPPEALKPTVIVAE
EDGNDGCVESDSLRSNRQKRDARRAVKWMELASFSGDOVKQILKAASLGEVYDAL
MLAKRLGSDVRECKRRHFNYLIGKLLREVEPLMDTLINATKQGDHSTLQTLISSAKOV
ADDVGDSTDDDTETESEDEEGSDEYTAMAAWFEDGLISQNVELTKVEYLSQSVDFOR
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatgagaa 1979
|||||
Db 131163 TATGTTCAACATAAGATGATGAGAA 131138

RESULT 8
VSNER VSNER 2641 bp mRNA PLN 14-SEP-1993
LOCUS V.sativa mRNA for NADPH-ferrihemoprotein reductase.
ACCESSION Z26252
VERSION Z26252.1 GI:400531
KEYWORDS NADPH-ferrihemoprotein reductase.
SOURCE spring vetch.
ORGANISM Vicia sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Vicia.
REFERENCE 1 (bases 204 to 2282)
AUTHORS Benveniste,I., Begue-Kirn,C., Lesot,A., Hasenfratz,M. and Durst,F.
TITLE Isolation and characterization of a cDNA encoding an
NADPH-cytochrome P450 reductase from Vicia sativa
JOURNAL Unpublished
AUTHORS Durst,F.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-1993) Durst F., CNRS - Institut de Biologie
Moléculaire des Plantes, Cellular and Molecular Enzymology, 28, rue
Goethe, Strasbourg, France, F-67083
FEATURES
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1. 2641
/organism="Vicia sativa"
/strain="Var. lolita"
/db_xref="taxon:3908"
/clone="9a13c"
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/clone_lib="lambda Zap library of I. Benveniste"
/dev_stage="7 day dark-grown seedlings"
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/function="Catalyzes the reduction of cytochrome P450 in
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WFTGKEERGTLQQLTYGVFALGNRQYHFHNKIVDEDLTEQGAKRLLVPVGLGDD
QSDIEDFNWAKETLWPELDQLRDEDDVNTASTPYTAAISEYRVV IHDPTVSPSYEN
HFNVANGAVYEDIHPCRVNVAVRRELHKPQSDRSCIHLEFDLSGTGVTYETGDHGV
YAENCNDEVEAGKLLGQSLDLLFLSHTDKEDGTSLSGSLPPPGPCTVRTALACVA
DLNPPKRAIVALAAHASEPSEARLKFLLSSPGQKDEYSKWVVGORSLLLEWADFP
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WMSKATPLEKSHDCSRAPIRFSPNFKLPADHSIPIIMVGPGLAPFRGLQERLAL
KEDGVQLGALLFFGCRNQMDFIYEDLNNVQQAISELIVAFSREGPEYVQHK
MMDKAEYLWSLISGGYLYCGDAKGARDVHRSLSHTIVQQQENADSSKAEATVKKIQ
MDGRYLRDVM"
713 a 511 c 615 g 802 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 24; DB 9; Length 129332;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 tggctactcagactggtactgtgta 398
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Db 464 TGCTACTCAGACTGCTACTGCTGA 487

RESULT 9
AL590028 129332 bp DNA PRI 09-MAY-2001
LOCUS Human DNA sequence from clone RP11-384M8 on chromosome 13, complete
sequence.
ACCESSION AL590028
VERSION AL590028.7 GI:14018310
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 129332)
AUTHORS Peck,A.
TITLE Direct Submission
JOURNAL Submitted (09-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On May 11, 2001 this sequence version replaced GI:13990191.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C-elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-384M8 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-384M8. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-131P10 is at 129333 in this
sequence. The true right end of clone RP11-196I2 is at 100 in this
sequence.
FEATURES
source
1. 129332
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/db_xref="taxon:9606"
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ORIGIN

Query Match
Best Local Similarity 100.0%; Score 24; DB 9; Length 129332;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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misc_feature 1936. .21856
/feature="assembly_name:Contig33
clone_end:T7"
misc_feature 21757. .163603
/feature="assembly_name:Contig34
clone_end:SP6"
BASE COUNT 56206 a 29637 c 28754 g 48804 t 202 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2626 agagttttgagaaaaa 2649
|||||
Db 43242 AGAGTTTGGAGAAAAA 43265
|||||

RESULT 12
BC011090 1864 bp mRNA ROD 30-JUL-2001
LOCUS Mus musculus, Similar to DnaJ (Hsp40) homolog, subfamily B, member
DEFINITION 10. clone MGC:19256 IMAGE:3968468, mRNA, complete cds.
ACCESSION BC011090
VERSION BC011090.1 GI:15029742
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1864)
Strausberg,R.
Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalobebcm.tmc.edu.
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 23 Row: j Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction, Similarity but not identity
to protein.
FEATURES
source 1. .1864
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/db_xref="taxon:10090"
/clone="MGC:19256 IMAGE:3968468"
/tissue_types="Mammary tumor. Metallothionien-TGF alpha
model. 10 month old virgin mouse. Taken by biopsy."
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102. .935
CDS

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AGAFRSVSTSTTFVQGRITTRIMENGQERVEEDGQLKSVINSINGVDDLAIGLEL
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F"
BASE COUNT 427 a 458 c 541 g 438 t
ORIGIN
Query Match 0.9%; Score 23; DB 10; Length 1864;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2627 gagtttgagaaaaa 2649
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Db 1812 GAGTTTGGAGAAAAA 1834
|||||

RESULT 13
AF024634 2456 bp mRNA PLN 26-JAN-1998
LOCUS Petroselinum crispum NADPH cytochrome P450 reductase (CPR2) mRNA,
DEFINITION complete cds.
ACCESSION AF024634
VERSION AF024634.1 GI:2809384
KEYWORDS parsley.
SOURCE Petroselinum crispum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
1 (bases 1 to 2456)
Koopmann,E. and Hahlbrock,K.
Differentially regulated NADPH:cytochrome P450 oxidoreductases in
parsley
Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14954-14959 (1997)
98070859
REFERENCE 2 (bases 1 to 2456)
AUTHORS Koopmann,E. and Hahlbrock,K.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (12-SEP-1997) Biochemistry, Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln 50829, Germany
Location/Qualifiers
1. .2456
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BASE COUNT 660 a 474 c 617 g 715 t
ORIGIN ISEGAYIVCGDAKGHARDVHRLMHTIAEQGALDSSKAESWYKNLQMTGRYLDRDWM"

Query Match 0.9% Score 23; DB 8; Length 2466;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 763 gatgatcaatgcatggaatga 785
|||||
Db 697 GATGATCAATGCAATGGAATGA 719

RESULT 14
AF002698
LOCUS Pisum sativum putative NADPH-cytochrome P450 reductase (PSC450R1)
DEFINITION mRNA, complete cds.
ACCESSION AF002698
VERSION AF002698.2 GI:6503252
KEYWORDS
SOURCE pea.
ORGANISM Pisum sativum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.
1 (bases 1 to 2545)
Brosche,M., Fant,C., Bergkvist,S.W., Strid,H., Svensk,A., Olsson,O.
and Strid,A.

TITLE Molecular markers for UV-B stress in plants: alteration of the
expression of four classes of genes in pisum sativum and the
formation of high molecular mass RNA adducts(1)

JOURNAL Biochim. Biophys. Acta 1447 (2-3), 185-198 (1999)
MEDLINE 20011276
PUBMED 10542315
REFERENCE 2 (bases 387 to 538)
AUTHORS Strid,A. and Brosche,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-1997) Biochemistry and Biophysics, Goteborg
University, Lundberg Laboratory, Medicinaregatan 9c, Goteborg
S-41390, Sweden
3 (bases 387 to 538)
Strid,A. and Brosche,M.
Direct Submission
Submitted (02-APR-1998) Biochemistry and Biophysics, Goteborg
University, Lundberg Laboratory, Medicinaregatan 9c, Goteborg
S-41390, Sweden

REMARK Sequence update by submitter
REFERENCE 4 (bases 1 to 2545)
AUTHORS Strid,A. and Brosche,M.
TITLE Direct Submission
JOURNAL Submitted (02-Dec-1999) Biochemistry and Biophysics, Goteborg
University, Lundberg Laboratory, Medicinaregatan 9c, Goteborg
S-41390, Sweden
REMARK Sequence update by submitter
COMMENT On Dec 2, 1999 this sequence version replaced gi:3006199.
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/cultivar="Greenfeast"
/db_xref="taxon:3888"
/tissue_type="leaf"
/note="expression was confirmed by hybridisation to
Northern blots"
1. .2545
/gene="PSC450R1"
111. .2225
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gene
CDS
/note="sequence name: MB19; similar to Arabidopsis
thaliana NADPH-cytochrome P450 reductase encoded by the
sequence presented in the file with GenBank Accession

Number X66017"
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GKRLVPVGLGDDQCIEDFTAWKELEPALDQLLDEDDTVPATPYTAASVYRV
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ORSLLIEGVCSFTWKNVPLEKQDCSWAPFVRSNFRPLADNKVPVIMIGPCTGLA
PFRGLQERLALKEGAEGLPSVLFQGRNRQVDYIYEDELNHFVNGGALSSELIVAFS
RDGPTKEYVOHKMKERASDJWNMISOGAYVYVCGDAKGMARDVHRTLHTILQEQSLD
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BASE COUNT 721 a 487 c 585 g 752 t
ORIGIN

Query Match 0.9% Score 23; DB 8; Length 2545;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2023 tatgtgtgtgtgatgccaaagg 2045
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Db 2073 TATGTGTGTGTGTCGCAAGGG 2095
|||||

RESULT 15
VIRNADPHP4
LOCUS 2617 bp mRNA PLN 23-APR-2001
DEFINITION Vigna radiata NADPH cytochrome P450 mRNA, complete cds.
ACCESSION L07843
VERSION L07843.1 GI:295447
KEYWORDS
SOURCE Vigna radiata.
ORGANISM Vigna radiata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vigna.
1 (bases 1 to 2617)
Shet,M., Sathasivan,K., Mehdy,M., Arlotto,M. and Estabrook,R.
Purification, characterization and cDNA cloning of NADPH-cytochrome
P450 reductase from mung bean
Proc. Natl. Acad. Sci. U.S.A. 90, 2890-2894 (1993)
93219390

FEATURES Location/Qualifiers
1. .2617
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/dev_stage="7 day etiolated seedling 15 hr after wounding"
1. .174
175. .2247
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KNAIPSEKSDQSSAPIFIRPSNFKLPVDHSPIIIVMGPTGLAPRFGFQERTALKE
DGVOLGPALLFFQGRNRQMDFIYEDELKSEVQGSSELIVAFSRGAERKEYVQHKMM
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5'UTR
CDS
/note="sequence name: MB19; similar to Arabidopsis
thaliana NADPH-cytochrome P450 reductase encoded by the
sequence presented in the file with GenBank Accession


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3'UTR          GRYLRDVM
2245. .2617
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BASE COUNT    668 a 512 c 622 g 815 t
ORIGIN

Query Match      0.9%; Score 23; DB 8; Length 2617;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 463 gttgacctggtgactatgcagc 485
    |||||||||||||||||||
Db 520 GTTGACCTGGATGACTATGCAGC 542

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Search completed: December 27, 2001, 16:27:54
Job time: 14099 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 14:12:15 ; Search time 222.02 Seconds
(without alignments)
10229.054 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcgagctgttagtat.....tttgagaaaaaaaaaaaaa 2649

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_1101.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2547	96.1	2650	20 AAX08517	Poppy cytochrome P
2	26	1.0	2114	14 AAO51236	Plant NADPH cytoch
3	22	0.8	600	21 AAC98382	Human colon cancer
4	21	0.8	4507	16 AAO83525	SABP gene. Plasm
5	21	0.8	4507	18 AA72888	Sialic acid bindin
6	21	0.8	4507	21 AA298282	P. falciparum SAPP
7	20	0.8	306	21 AAC74719	Human ORFX ORF274
8	20	0.8	485	21 AAC35800	Zea mays DNA fragm
9	20	0.8	531	21 AAA46546	CDNA sequence enco
10	20	0.8	1173	21 AAC43163	Arabidopsis thalia
11	20	0.8	1695	21 AAC49051	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAX08517
ID AAX08517 standard; DNA: 2650 BP.
XX AC AAX08517;
DT 19-JUL-1999 (first entry)
XX DE Poppy cytochrome P450 reductase.
XX KW Oplum poppy; alkaloids; cytochrome P450 reductase; morphine;
KW codeine; oripavine; thebaine; transformation; crop yield; probe;
KW primer; ss.
XX OS Papaver somniferum.
XX FH Key Location/Qualifiers
CDS 124..2175
FT /*tag= a
FT /product= "Cytochrome P450 reductase"
XX PN WO9911765-A1.
XX PD 11-MAR-1999.
XX PF 28-AUG-1998; 98WO-AU00705.
XX PR 29-AUG-1997; 97AU-0008872.
XX PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX PI Atkins DG, Fist AJ, Kutchan TM, Zenk MH;
XX WPI; 1998-214703/18.

12	20	0.8	2136	21 AAC44709	Arabidopsis thalia
13	20	0.8	2558	20 AAX08520	Poppy cytochrome P
14	20	0.8	2792	21 AAA26994	Maize PCNA p120 ge
15	20	0.8	4101	22 AAS11602	Mouse cDNA encodin
16	19	0.7	623	21 AAA44664	Human secreted exp
17	19	0.7	925	18 AAT89370	Neospora caninum a
18	19	0.7	1087	21 AAC39331	Arabidopsis thalia
19	19	0.7	1209	21 AAC34228	Arabidopsis thalia
20	19	0.7	1302	21 AAC51430	Arabidopsis thalia
21	19	0.7	1554	22 AAF80406	Nucleotide sequenc
22	19	0.7	1613	21 AAA46500	cDNA encoding enzy
23	19	0.7	1651	18 AAT97300	Streptococcus pneu
24	19	0.7	1783	22 AAH73271	A novel pros polyn
25	19	0.7	1783	22 AAH73271	Human cervical can
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27	19	0.7	1880	22 AAH16945	Human cDNA sequenc
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29	19	0.7	2445	19 AAT98579	DNA encoding a S.
30	19	0.7	2801	22 AAF32643	Human cDNA encodin
31	19	0.7	3044	20 AAX81125	Senescence-associa
32	19	0.7	3370	21 AAA16630	Human secreted pro
33	19	0.7	3463	21 AAT78074	Human cancer assoc
34	19	0.7	4694	19 AA296274	S. pneumoniae deri
35	19	0.7	4694	19 AA296274	Streptococcus pneu
36	19	0.7	9990	22 AAH26123	Mouse prion protei
37	19	0.7	9990	22 AAH26136	Mouse PrP/human ta
38	19	0.7	49136	21 AAA27475	NIDDM1 region incl
39	19	0.7	50000	21 AAA96364	Polymorphic repeat
40	18	0.7	334	22 AAS02562	DNA encoding prope
41	18	0.7	340	22 AAS02561	DNA encoding prope
42	18	0.7	367	22 AAS02563	DNA encoding prope
43	18	0.7	378	22 AAS02191	DNA encoding prope
44	18	0.7	379	19 AAV20508	Conus lynceus cona
45	18	0.7	379	19 AAV17137	Conus lynceus cona

DR P-PSDB; AAW85680, AAW85682.
XX Nucleic acid encoding cytochrome P-450 reductase from poppy
PT Claim 3; Fig 9a; 58pp; English.
XX
CC Transforming plants with a nucleic acid molecule encoding cytochrome
CC P450 reductase alters the yield and/or type of alkaloids produced.
CC In opium poppies it specifically increases the yield of medically
CC useful alkaloids such as morphine, codeine, oripavine and thebaine.
CC Sequences complementary to the coding sequence of cytochrome P450
CC reductase are useful as probes, primers and antisense sequences, or
CC for design of ribozymes. Transformation with DNA encoding the
CC cytochrome P450 reductase allows regulation of the total alkaloid
CC content and of the relative proportions of individual alkaloids.
CC produced. Increasing the alkaloid content of poppy straw should
CC reduce the cost of alkaloid production. Cytochrome P450 reductase
CC is the rate-limiting enzyme in biosynthesis of alkaloids in poppies.
CC Peptide fragments of the cytochrome P450 reductase are described in
CC AAW85672-W85678.
XX
SQ Sequence 2650 BP; 766 A; 514 C; 606 G; 764 T; 0 other;

Query Match 96.1%; Score 2547; DB 20; Length 2650;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2647; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 61 cgaatctacttgaaatacattcgattgcttctctctgttttaagcttcagagctctgcta 120
Dy 61 cgaatctacttgaaatacattcgattgcttctctctgttttaagcttcagagctctgcta 120

Qy 121 attatgggttcgaataatttagtaattcgattgaatcgatggttaggaataatcaatgga 180
Dy 121 attatgggttcgaataatttagtaattcgattgaatcgatggttaggaataatcaatgga 180

Qy 181 tcagaataatttctgacccaattttcattatggttcacaaactgtagcttcaatgctgatt 240
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Qy 301 tataaaccataattgataaagagaagagagagattgaagtgtgatcctggtataaattaaag 360
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Qy 361 ctcaactatatttttggctacagactggtactgctgaagatttgcataaggcattggcca 420
Dy 361 ctcaactatatttttggctacagactggtactgctgaagatttgcataaggcattggcca 420

Qy 421 gaagaataaaggcaagtaacagaagaagcagttgtttaagtagttgacctggatgactat 480
Dy 421 gaagaataaaggcaagtaacagaagaagcagttgtttaagtagttgacctggatgactat 480

Qy 481 gcagccgagatgatcaatatgaagagaataataagaagaagctcttgggttttttcattg 540
Dy 481 gcagccgagatgatcaatatgaagagaataataagaagaagctcttgggttttttcattg 540

Qy 541 gtgaccacttatggtggtgagcccaactgacaatgctgcgagattttacaaatgggttc 600
Dy 541 gtgaccacttatggtggtgagcccaactgacaatgctgcgagattttacaaatgggttc 600

Qy 601 actcaggaacatgaaggggagagtgcttcagcaactaacttatggttttgggttg 660
Dy 601 actcaggaacatgaaggggagagtgcttcagcaactaacttatggttttgggttg 660

Qy 661 ggtaacgctcaatcagcagcatttcaacaagatcgcggttagatgtggtgagcgaactcggt 720

Db 661 ggtaacgctcaatcagcagcatttcaacaagatcgcggttagatgtggatgagcaaacctcggt 720
Qy 721 aacaaggtgcaaaagcgcatgtttcaagtggggctcggtgacgatgatcaatgattgaa 780
Dy 721 aacaaggtgcaaaagcgcatgtttcaagtggggctcggtgacgatgatcaatgattgaa 780

Qy 781 gatattttactgcttggcgagaattgttggactgaattggatcagttcgtctcaaaagt 840
Dy 781 gatattttactgcttggcgagaattgttggactgaattggatcagttcgtctcaaaagt 840

Qy 841 gagatgctgctcttcagttggtcacaccgtatatgtctactgttccctgaatacagggtta 900
Dy 841 gagatgctgctcttcagttggtcacaccgtatatgtctactgttccctgaatacagggtta 900

Qy 901 gtgattcacaagaactacggtcgcggctctggtatgataaacaacataaatactgtaacggc 960
Dy 901 gtgattcacaagaactacggtcgcggctctggtatgataaacaacataaatactgtaacggc 960

Qy 961 gatgttcatttgatatctccatcctcttgagaaccattgttgcacaacaagagagctc 1020
Dy 961 gatgttcatttgatatctccatcctcttgagaaccattgttgcacaacaagagagctc 1020

Qy 1021 cacaacccaagtctgatatcctctgtatacatctggagttcgacatatcaggtctctcc 1080
Dy 1021 cacaacccaagtctgatatcctctgtatacatctggagttcgacatatcaggtctctcc 1080

Qy 1081 cttacatatgagactggagatcattgttgggttttatgtcgtagaactgcgtagaaactgtc 1140
Dy 1081 cttacatatgagactggagatcattgttgggttttatgtcgtagaactgcgtagaaactgtc 1140

Qy 1141 gaggaagcagggaagctgttgggtcaacccctggatttgcgtttttcaattcacacggat 1200
Dy 1141 gaggaagcagggaagctgttgggtcaacccctggatttgcgtttttcaattcacacggat 1200

Qy 1201 aaagaagaagcgggtcacccacagggaagctcattaccacctcttcccaggtccttgcacc 1260
Dy 1201 aaagaagaagcgggtcacccacagggaagctcattaccacctcttcccaggtccttgcacc 1260

Qy 1261 ttacgatctgccccctagcacgctatgctgatttttgaatcctcctagaaagctctctg 1320
Dy 1261 ttacgatctgccccctagcacgctatgctgatttttgaatcctcctagaaagctctctg 1320

Qy 1321 attgctctgctcgctcatgcatctgtaccagtgaaagcagagagattgcgtttttgtcca 1380
Dy 1321 attgctctgctcgctcatgcatctgtaccagtgaaagcagagagattgcgtttttgtcca 1380

Qy 1381 tcacctctgggaagaatgagatttcaaaatgggttagttggaagtacagagagctctttg 1440
Dy 1381 tcacctctgggaagaatgagatttcaaaatgggttagttggaagtacagagagctctttg 1440

Qy 1441 gagatcatggccgagtttccatcagcaaaacccctcttgggtgttcttctgtcgcagta 1500
Dy 1441 gagatcatggccgagtttccatcagcaaaacccctcttgggtgttcttctgtcgcagta 1500

Qy 1501 gccctcgcttacgcgctcgatactattctatctcatcctcctcctaagtgttgcctcca 1560
Dy 1501 gccctcgcttacgcgctcgatactattctatctcatcctcctcctaagtgttgcctcca 1560

Qy 1561 agaattcattgtgacgctgtgcttttagtataatggtcaaaagccctaccggaaggttcaccca 1620
Dy 1561 agaattcattgtgacgctgtgcttttagtataatggtcaaaagccctaccggaaggttcaccca 1620

Qy 1621 ggaagtgttgcacatggatgaacatcagttcctcctcaggtagctgggctcctctattttt 1680
Dy 1621 ggaagtgttgcacatggatgaacatcagttcctcctcaggtagctgggctcctctattttt 1680

Qy 1681 gttcgaacgtcaaaacttcaagtaccagctaccctcaactccaatttatcatggtggga 1740
Dy 1681 gttcgaacgtcaaaacttcaagtaccagctaccctcaactccaatttatcatggtggga 1740

Qy 1741 cctggtacaggggttagctccttctcagagagatttctgcagggaagaatggcctcaagaa 1800
Dy 1741 cctggtacaggggttagctccttctcagagagatttctgcagggaagaatggcctcaagaa 1800

Db 1741 cctggtacagggttagctctctttccagaggattttctgcaggaaagaattgcccctcaaggaa 1800
Qy 1801 aatggtctcaactgcccagcagctctcttttcgagtaggaatcgtaatatgac 1860
Db 1801 aatggtctcaactgcccagcagctctcttttcgagtaggaatcgtaatatgac 1860
Qy 1861 ttcatttatgaagcgaactaaacaacttcgtggaacgagagtcatttcggagctagtt 1920
Db 1861 ttcatttatgaagcgaactaaacaacttcgtggaacgagagtaatttcggagctagtt 1920
Qy 1921 attgctctttcacgtgaagggaagaaagaagaatatattcaacataagatgagagaaa 1980
Db 1921 attgctctttcacgtgaagggaagaaagaagaatatattcaacataagatgagagaaa 1980
Qy 1981 gcaacgagatgatggaatgtagatcagggagacggttatctctatgtgtgtggtgagcc 2040
Db 1981 gcaacgagatgatggaatgtagatcagggagacggttatctctatgtgtgtggtgagcc 2040
Qy 2041 aagggaatgccagagatgtccatcgcaagtgtgcataccattgcccaagaacaggagacc 2100
Db 2041 aagggaatgccagagatgtccatcgcaagtgtgcataccattgcccaagaacaggagacc 2100
Qy 2101 atggaatcaatctgctgcgaagctgcagtaaaagaacatccaagttagaagacgatatcta 2160
Db 2101 atggaatcaatctgctgcgaagctgcagtaaaagaacatccaagttagaagacgatatcta 2160
Qy 2161 agagatgctggtgtagcgaatgtagctgtccaaagtcacctttcttggtggtctgttta 2220
Db 2161 agagatgctggtgtagcgaatgtagctgtccaaagtcacctttcttggtggtctgttta 2220
Qy 2221 tggttctattatattatgattcctctctgaaatcccaagcacttccagacatccctc 2280
Db 2221 tggttctattatattatgattcctctctgaaatcccaagcacttccagacatccctc 2280
Qy 2281 gattcttccctcagtggttccaaatcgaaagctcggtataattgagagcagtgcaattgtg 2340
Db 2281 gattcttccctcagtggttccaaatcgaaagctcggtataattgagagcagtgcaattgtg 2340
Qy 2341 actacatgagaagcaaacatcgataccatagaaatgagaagatcaaaattctctatca 2400
Db 2341 actacatgagaagcaaacatcgataccatagaaatgagaagatcaaaattctctatca 2400
Qy 2401 gaacaatgttacaggcaaaactggttctgcttaataataatctcacaccatgggtgtgga 2460
Db 2401 gaacaatgttacaggcaaaactggttctgcttaataataatctcacaccatgggtgtgga 2460
Qy 2461 caacactgaaacagcatatagctataccaaacaaagttatgcaagaaacacaaactagta 2520
Db 2461 caacactgaaacagcatatagctataccaaacaaagttatgcaagaaacacaaactagta 2520
Qy 2521 gatcttctcttgattgattactgttaagttcttaaccagatgataagttgacttaaga 2580
Db 2521 gatcttctcttgattgattactgttaagttcttaaccagatgataagttgacttaaga 2580
Qy 2581 tctctgtttctctatggtctaccgagagagtagtatataatgcatttagagttttgagaaaa 2640
Db 2581 tctctgtttctctatggtctaccgagagagtagtatataatgcatttagagttttgagaaaa 2640
Qy 2641 aaaaaaaaaa 2649
Db 2641 aaaaaaaaaa 2649

RESULT 2
AAQ51236
ID AAQ51236 standard; cDNA; 2114 BP.
XX AC
XX AAQ51236;
DT 11-MAY-1994 (first entry)
XX Plant NADPH cytochrome P450 reductase (ara B).
DE
XX

KW NADPH cytochrome P450 reductase; functional complementation;
KW identification; ss.
XX Arabidopsis thaliana.
OS
FH Key Location/Qualifiers
FT CDS 36..2114
FT /tag= a
FT /product= NADPH cytochrome P450 reductase.
FT misc_difference 510..512
FT /tag= c
FT /transl_except= AGA encodes Lys.
FT misc_difference 543..545
FT /tag= d
FT /transl_except= CGG encodes Lys.
FT misc_difference 663..665
FT /tag= e
FT /transl_except= CGT encodes Lys.
FT misc_difference 819..821
FT /tag= f
FT /transl_except= CGG encodes Lys.
FT misc_difference 915..917
FT /tag= g
FT /transl_except= AGG encodes Lys.
FT misc_difference 1203..1205
FT /tag= j
FT /transl_except= AGA encodes Lys.
FT misc_difference 1230..1232
FT /tag= k
FT /transl_except= CGA encodes Lys.
FT misc_difference 1431..1433
FT /tag= l
FT /transl_except= CGT encodes Lys.
FT misc_difference 1443..1445
FT /tag= m
FT /transl_except= CGT encodes Lys.
FT misc_difference 1484..1486
FT /tag= n
FT /transl_except= AGA encodes Lys.
FT misc_difference 1533..1535
FT /tag= o
FT /transl_except= AGA encodes Lys.
FT misc_difference 1623..1625
FT /tag= p
FT /transl_except= CGA encodes Lys.
FT misc_difference 1704..1706
FT /tag= q
FT /transl_except= AGA encodes Lys.
FT misc_difference 1782..1784
FT /tag= p
FT /transl_except= AGA encodes Lys.
FT misc_difference 1788..1790
FT /tag= q
FT /transl_except= CGA encodes Lys.
FT misc_difference 1872..1874
FT /tag= r
FT /transl_except= CGT encodes Lys.
FT misc_difference 1992..1994
FT /tag= s
FT /transl_except= AGG encodes Lys.
FT misc_difference 2004..2006
FT /tag= t
FT /transl_except= CGA encodes Lys.
FT misc_difference 2091..2093
FT /tag= u
FT /transl_except= AGA encodes Lys.
FT misc_difference 2100..2102

FT /*tag= v
 FT /transl_except= AGA encodes Lys.

PN WO9321326-A.
 XX
 XX 28-OCT-1993.
 PD
 XX
 XX 13-APR-1993; 93WO-FR00367.
 PF
 XX
 XX 13-APR-1992; 92FR-0004491.
 PR
 XX
 XX (ORSA-) ORSAN.
 PA
 XX
 XX Kazmaier M, Lacroute F, Mignotte-vieux C, Minet M;
 PI Pompon D;
 PI
 XX

DR WPI; 1993-351736/44.
 DR P-PSDB; AAR43581.
 XX
 XX New DNA encoding plant NADPH cytochrome P450 reductase - cloned
 PT by functional complementation in yeast, also recombinant enzyme
 PT useful in P450 mediated bioconversion processes
 XX

XX Claim 11; Figure 9; 79pp; French.

PS A new method for determining whether a DNA sequence encodes an NADPH
 CC cytochrome P450 reductase involves transforming yeasts with plasmids
 CC of a total cDNA bank of plant(s). The yeasts used in the procedure
 CC are incapable of producing their own NADPH cytochrome P450
 CC reductase. They are then exposed to a cytochrome P450 inhibitor at a
 CC level which is lethal to the yeast cells but not to cells which,
 CC because of the transformation, now contain an active NADPH
 CC cytochrome P450 reductase. Surviving clones are then isolated and
 CC plasmid DNA extracted. The gene is inserted into the plasmid at a
 CC site which places it under the control of an inducible promoter.
 XX

SQ Sequence 2114 BP; 603 A; 400 C; 542 G; 569 T; 0 other;

Query Match 1.0%; Score 26; DB 14; Length 2114;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1954 tatgttcaacataagatgatggagaa 1979
 |||||
 Db 1893 tatgttcaacataagatgatggagaa 1918

RESULT 3
 AAC98382
 ID AAC98382 standard; CDNA; 600 BP.

XX
 AC AAC98382;

XX 09-MAR-2001 (first entry)

XX Human colon cancer antigen nucleotide sequence SEQ ID NO:392.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder; ss.

XX Homo sapiens.

XX WO200055351-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05883.

XX 12-MAR-1999; 99US-0124270.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM;
 PI
 XX WPI; 2000-587534/55.
 DR P-PSDB; AAB53625.

XX Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -

XX Claim 1; Page 856; 2104pp; English.

XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 600 BP; 194 A; 128 C; 140 G; 131 T; 7 other;

Query Match 0.8%; Score 22; DB 21; Length 600;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 498 atatgaagagaaattaaagaaa 519
 |||||

Db 435 atatgaagagaaattaaagaaa 456

RESULT 4

AAC983525
 ID AAC983525 standard; DNA; 4507 BP.

XX
 AC AAC983525;

XX 22-SEP-1995 (first entry)

XX SABP gene.

XX SABP; sialic acid binding protein; binding domain; merozoite;
 KW malaria; therapy; vaccine; ss.

XX Plasmodium falciparum.

XX WO9507353-A.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10230.

XX 10-SEP-1993; 93US-0119677.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Chitnis C, Miller LH, Peterson DS, Sim KL, Su X;

XX Wellem's TE;

DR WPI: 1995-123427/16.
 XX P-PSDB; AAR70232.
 XX
 PT New erythrocyte binding domain polypeptide(s) - isolated from
 PT Plasmodium binding proteins, used in diagnosis, treatment and
 PT prevention of malaria
 XX
 PS Disclosure: Page 39-41; 81pp; English.
 XX
 CC Sequences from the SABP gene (given in AA083525) were PCR amplified,
 CC expressed on the surface of COS cells and tested for erythrocyte
 CC binding to identify the binding domain polypeptide. A prefd. SABP
 CC binding domain comprises residues 1 to about 616 of the SABP protein
 CC (AAR70232). Recombinant binding domain was expressed in E. coli,
 CC yeast, mammalian, insect, and in vaccinia virus and adenovirus-
 CC infected cells. It provides protection against P. falciparum.
 XX
 SQ Sequence 4507 BP; 1955 A; 458 C; 796 G; 1298 T; 0 other;

Query Match 0.8%; Score 21; DB 16; Length 4507;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1987 gatgtatggaatgtgatca 2007
 |||||
 Db 1853 gatgtatggaatgtgatca 1873
 |||||

RESULT 5
 AAT72888
 ID AAT72888 standard; DNA; 4507 BP.
 XX
 AC AAT72888;
 XX
 DT 11-SEP-1997 (first entry)
 XX
 XX Sialic acid binding protein coding sequence.
 XX
 DE DBL gene family; SABP; sialic acid binding protein; merozoite; malaria;
 KW Duffy antigen binding protein; DABP; erythrocyte; var-1; var-2; var-3;
 KW var-7; vaccine; therapy; immune response; Plasmodium; ss.
 KW
 XX Plasmodium falciparum.
 OS
 XX
 XX Key Location/Qualifiers
 FH 56..4363
 FT CDS /*tag= a
 FT /product= Duffy antigen binding protein
 XX
 XX WO9640766-A2.
 XX
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US09508.
 XX
 XX 07-JUN-1995; 95US-0487826.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Chitnis C, Miller LH, Peterson DS, Sim KL, Su X;
 PI Wellem's TE;
 XX
 XX WPI: 1997-052231/05.
 DR P-PSDB; AAW22477.
 XX
 XX New malaria vaccines - contains cysteine-rich DBL family protein
 PT binding domains homologous domains of the Duffy and sialic acid
 PT binding proteins
 XX
 XX Example 1; Page 35-36; 96pp; English.
 PS
 XX This sequence represents the full length coding sequence for the sialic

CC acid binding protein (SABP). SABP and the Duffy antigen binding protein
 CC (DABP) are soluble proteins that appear in the culture supernatant after
 CC infected erythrocytes release merozoites. DABP and SABP mediate the
 CC binding of merozoites and schizonts to the erythrocyte surface. These
 CC proteins are necessary for erythrocyte invasion by the parasite. This
 CC sequence can be used in the compositions of the invention. The
 CC compositions are for the treatment and prevention of malaria, and
 CC comprise either a nucleotide sequence or encoded polypeptide of the
 CC var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of
 CC genes having homology with conserved regions of DABP and SABP. The
 CC compositions are used for the treatment and prevention of malaria. They
 CC are also used in the preparation of vaccines for inducing a protective
 CC immune response in a mammal to Plasmodium merozoites (especially
 CC Plasmodium falciparum or Plasmodium vivax).
 XX
 SQ Sequence 4507 BP; 1955 A; 458 C; 796 G; 1298 T; 0 other;

Query Match 0.8%; Score 21; DB 18; Length 4507;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1987 gatgtatggaatgtgatca 2007
 |||||
 Db 1853 gatgtatggaatgtgatca 1873
 |||||

RESULT 6
 AAZ98282
 ID AAZ98282 standard; DNA; 4507 BP.
 XX
 AC AAZ98282;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE P. falciparum SABP binding domain polypeptide encoding DNA.
 XX
 KW DBL gene; Duffy-binding like gene; ebl-1; Duffy Antigen Binding Protein;
 KW DABP; Sialic Acid Binding Protein; SABP; malaria; vaccine; immunisation;
 KW protozoacide; ds.
 KW
 OS Plasmodium falciparum.
 XX
 XX US5993827-A.
 XX
 XX 30-NOV-1999.
 XX
 XX 07-JUN-1995; 95US-0487826.
 XX
 XX 10-SEP-1993; 93US-0119677.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Sim KL, Chitnis C, Peterson DS, Su X, Wellem's TE, Miller LH;
 PI WPI: 2000-194198/17.
 DR P-PSDB; AAY77900.
 XX
 XX Isolated protein binding domains from Plasmodium vivax and Plasmodium
 PT falciparum erythrocyte binding proteins useful for vaccinating against
 PT malaria -
 XX
 XX Example 1; Columns 39-44; 93pp; English.
 PS
 XX The invention relates to ebl-1 polypeptides that are encoded by the DBL
 CC (Duffy-binding like) gene family. The ebl-1 proteins are substantially
 CC identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid
 CC Binding Protein (SABP), which are soluble proteins that appear in the
 CC culture supernatant after erythrocytes infected with malaria release
 CC merozoites. Immunochemical studies indicate that DABP and SABP are the
 CC respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy
 CC and sialic acid receptors on erythrocytes. The ebl-1 polypeptides may be
 CC used to vaccinate against malaria, especially caused by P. falciparum.

CC Immunization with the polypeptide provides effective protection against
 CC malaria. The present sequence represents the SAPP binding domain
 CC polypeptide encoding DNA.

XX Sequence 4507 BP; 1955 A; 458 C; 796 G; 1298 T; 0 other;

Query Match 0.8%; Score 21; DB 21; Length 4507;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1987 gatgtatgaatgtgatca 2007
 |||||
 Db 1853 gatgtatgaatgtgatca 1873

RESULT 7

AAC74719
 ID AAC74719 standard; cDNA; 306 BP.

XX AAC74719;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF274 polynucleotide sequence SEQ ID NO:547.

XX Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disease; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.

XX Homo sapiens.

OS WO200058473-A2.

PN 05-OCT-2000.

PD 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

DR P-PSDB; AAB40510.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

PS Claim 5; Page 707; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;

CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 306 BP; 80 A; 59 C; 55 G; 101 T; 11 other;

Query Match 0.8%; Score 20; DB 21; Length 306;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1634 catggatgaagcatgcagtt 1653

|||||

Db 36 catggatgaagcatgcagtt 55

RESULT 8

AAC35800

ID AAC35800 standard; DNA; 485 BP.

XX AAC35800;

AC AAC35800;

DT 17-OCT-2000 (first entry)

XX Zea mays DNA fragment SEQ ID NO: 11470.

XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic;
 KW pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

OS EP1033405-A2.

PN 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 25-MAR-1999; 99US-0125788.

PR 29-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0126785.

PR 06-APR-1999; 99US-0127462.

PR 08-APR-1999; 99US-0128234.

PR 16-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-0129845.

PR 21-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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KW Potassium channel interactor; PCIP; potassium channel; epilepsy;
KW spinocerebellar ataxia; nervous system disorder; cardiovascular disorder;
KW transient outward current; ss.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
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XX WO200031133-A2.
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XX PD 02-JUN-2000.
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XX
XX (MILL) MILLENNIUM PHARM INC.
XX (AMHP) AMERICAN HOME PROD CORP.
XX
XX Rhodes K, Betty M, Ling H, An W;
XX
XX WPI: 2000-400043/34.
XX P-PSDB: AAY93480.
XX
XX New polynucleotide with homology to the sequence encoding phosphate
XX channel interacting protein useful in the treatment of e.g. epilepsy
XX and spinocerebellar ataxia -
XX
XX Claim 2; Fig 19; 306pp; English.
XX
XX The present sequence encodes a potassium channel interactor protein
XX (PCIP). The PCIP polypeptides bind to a potassium channel, modulate
CC
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CC the activity of a potassium channel protein, and/or modulate a potassium
CC channel mediated activity in a cell. The polynucleotides and
CC polypeptides are useful in the treatment of epilepsy, and
CC spinocerebellar ataxia, as well as nervous system related disorders and
CC cardiovascular disorders associated with abnormal transient outward
CC currents. They are also useful for identifying compounds which can
CC bind to and modulate the expression and function of the PCIP nucleic
CC acid molecules, and proteins.
XX
XX Sequence 531 BP; 174 A; 120 C; 115 G; 121 T; 1 other;
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PR 29-OCT-1999; 99US-0162142. 10-JUN-1999; 99US-0146389.
PR 29-OCT-1999; 99US-0162142. 10-JUN-1999; 99US-0147038.
PR 29-OCT-1999; 99US-0162142. 10-JUN-1999; 99US-0147204.
PR 29-OCT-1999; 99US-0162142. 10-JUN-1999; 99US-0147302.
PR 29-OCT-1999; 99US-0162142. 10-JUN-1999; 99US-0147192.
PR 29-OCT-1999; 99US-0162142. 10-JUN-1999; 99US-0147260.

Query Match 0.8%; Score 20; DB 21; Length 1173;
Best Local Similarity 100.0%; Pred. No. 19;
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Qy 673 tacgagcattccaacagat 692
Db 90 TACGAGCATTTCAACAGAT 71

RESULT 11
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AC AAC49051;
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XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 59743.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
FN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 04-MAY-1999; 99US-0132484.
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PR 01-JUN-1999; 99US-0137222.
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Query Match      0.8%; Score 20; DB 21; Length 1695;
Best Local Similarity 100.0%; Pred. No. 19;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 673 tacgagcatttcaacaagat 692
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Db 90 TACGAGCATTTCAACAGAT 71

RESULT 12
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ID AAC44709 standard; DNA; 2136 BP.
XX
AC AAC44709;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43838.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
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Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC AAX08520;
XX
DT 19-JUL-1999 (first entry)
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XX Poppy cytochrome P450 reductase.
XX
XX Opium poppy; alkaloids; cytochrome P450 reductase; morphine;
KW codeine; oripavine; thebaine; transformation; crop yield; probe;
KW primer; ss.
XX
OS Eschscholzia californica.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /product= "Cytochrome P450 reductase"
FT
PN W09911765-A1.
XX
XX 11-MAR-1999.
PD
XX 28-AUG-1998; 98WO-AU00705.
XX
XX 29-AUG-1997; 97AU-0008872.
XX
XX (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
PA
XX Atkins DG, Fist AJ, Kutchan TM, Zenk MH;
PI
XX WPI; 1999-214703/18.
DR P-PSDB; AAW85681, AAW85683.
XX
XX Nucleic acid encoding cytochrome P-450 reductase from poppy
PT
XX
PS Claim 3; Fig 9b; 58pp; English.
XX
XX Transforming plants with a nucleic acid molecule encoding cytochrome
CC P450 reductase alters the yield and/or type of alkaloids produced.
CC In opium poppies it specifically increases the yield of medically
CC useful alkaloids such as morphine, codeine, oripavine and thebaine.
CC Sequences complementary to the coding sequence of cytochrome P450
CC reductase are useful as probes, primers and antisense sequences, or
CC for design of ribozymes. Transformation with DNA encoding the
CC cytochrome P450 reductase allows regulation of the total alkaloid
CC content and of the relative proportions of individual alkaloids.
CC produced. Increasing the alkaloid content of poppy straw should
CC reduce the cost of alkaloid production. Cytochrome P450 reductase
CC is the rate-limiting enzyme in biosynthesis of alkaloids in poppies.
CC Peptide fragments of the cytochrome P450 reductase are described in
CC AAW85672-W85678.
XX
SQ Sequence 2558 BP; 750 A; 477 C; 592 G; 739 T; 0 other;

Query Match 0.8%; Score 20; DB 20; Length 2558;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 860 ctgaattggtcagttgctc 879

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XX
AC AAA26994;

DT 22-AUG-2000 (first entry)
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DE Maize PCNA P120 gene fragment #3.
XX
KW Maize; plant cell proliferation-associated protein;
KW proliferating cell nuclear antigen; cell division stimulation;
KW proliferative; transgenic plant; plant growth; co-suppression;
KW chimeric gene; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
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FT /product= "PCNA P120"
XX
PN W0200031269-A2.
XX
PD 02-JUN-2000.
PF 19-NOV-1999; 99WO-US27550.
XX
XX 20-NOV-1998; 98US-0109266.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Cahoon RE, Klein TM, Weng Z, Lowe KS;
XX
DR WPI; 2000-400079/34.
DR P-PSDB; AAY94310.
XX
XX Nucleic acids encoding proteins involved in plant cell division and
PT proliferation useful for identifying modulators of plant growth -
XX
PS Claim 2; Page 36-37; 43pp; English.
XX
XX The present sequence is a nucleic acid fragment which encodes
CC proliferating cell nuclear antigen (PCNA) P120, a plant cell
CC proliferation-associated protein from Zea mays. The entire sequence
CC was found in a clone designated p0115.cisme95r from a cDNA library made
CC from corn leaf and sheath meristem tissue. Chimeric genes containing the
CC present nucleic acid fragment can be introduced into monocots and dicots
CC to produce plants expressing transgenic PCNA P120. By choosing a suitable
CC promoter, the fragment can be overexpressed or expressed at certain
CC developmental stages or in certain tissues. Co-suppression or antisense
CC chimeric genes can also be introduced to produce plants with reduced or
CC eliminated gene expression, thus inhibiting cell division and
CC proliferation. The present sequence may also be used to transform E. coli
CC in order to produce high levels of the protein for analysis. The nucleic
CC acid and the protein it encodes may be used to stimulate plant growth and
CC cell division and proliferation and to identify modulators of cell
CC division and proliferation.
XX
SQ Sequence 2792 BP; 841 A; 511 C; 691 G; 749 T; 0 other;

Query Match 0.8%; Score 20; DB 21; Length 2792;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2630 ttttgagaaaaa 2649
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Db 2757 ttttgagaaaaa 2776

RESULT 15
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ID AAS11602 standard; cDNA; 4101 BP.
XX
AC AAS11602;

Search completed: December 27, 2001, 15:59:40
Job time: 6445 sec

DT 24-OCT-2001 (first entry)
XX DE Mouse cDNA encoding CRIM1 protein.
XX
XX CRIM-1; Mouse; human chromosome 2p21-16.3; ophthalmological;
KW neuroprotective; renal; osteopathic; dental; vulnerary; immunogen;
KW antibody; gene therapy; neurodegenerative disease; eye disorder;
KW cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;
KW tooth abnormality; wound; ss; S52.
XX
OS Mus sp.
XX
XX Location/Qualifiers
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FT sig_peptide 63...89 /*tag= b
FT mat_peptide 90...3172 /*tag= c
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XX WO200138519-A1.
XX PN
XX
XX 31-MAY-2001.
XX PD
XX
XX PF 24-NOV-2000; 2000WO-AU01435.
XX
XX PR 26-NOV-1999; 99AU-0004348.
XX
XX (UYQU) UNIV QUEENSLAND.
XX PA
XX PI Little M, Yamada T, Holmes G, Georgas K, Kolle G, Wilkinson L;
XX
XX WPI; 2001-343951/36.
XX DR P-PSDB; AAU07142.
XX
XX Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,
PT useful for preventing, diagnosing and treating e.g. eye disease,
PT especially cataract formation -
XX
XX Claim 3; Fig 2; 169pp; English.
XX
XX The invention relates to nucleic acids from human chromosome 2p21-16.3
CC and the encoded peptide (and mouse and chicken orthologues) that
CC comprises a pEECCPLP group, an insulin-like growth factor binding protein
CC (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group
CC and a transmembrane domain. The protein, e.g. CRIM1, interacts with
CC peptides of the transforming growth factor superfamily. A composition
CC comprising an expression construct comprising the nucleic acids of the
CC invention or a mimetic which antagonises or mimics an activity of a CRIM1
CC polypeptide may be used in a method for modulating the biological
CC activity of a polypeptide of the bone morphogenic protein (BMP) family.
CC In this way they may be used to prevent or treat an eye disease,
CC especially cataract formation. They may also be used to treat
CC neurodegenerative diseases, renal and kidney disease, bone and tooth
CC abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
CC gene therapy by using antibodies directed against CRIM1 polypeptides.
CC The present sequence encodes mouse CRIM1 (AKA S52).
XX
XX Sequence 4101 BP; 967 A; 1067 C; 1154 G; 911 T; 2 other;

Query Match 0.8%; Score 20; DB 22; Length 4101;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2630 ttctgagaaaaaa 2649
Db 4077 ttctgagaaaaaa 4096

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 13:07:50 ; Search time 82.71 Seconds
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7253.539 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 351203 seqs, 11328999 residues

Word size : 0

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	0.8	4507	2	US-08-568-459A-3
2	21	0.8	4507	2	US-08-487-8268-3
C 3	19	0.7	1651	2	US-08-844-058-1
C 4	19	0.7	49136	4	US-09-422-869-1
C 5	18	0.7	379	4	US-09-142-078-57
C 6	18	0.7	379	4	US-09-357-141-57
C 7	18	0.7	394	4	US-09-142-078-53
C 8	18	0.7	394	4	US-09-357-141-53
C 9	18	0.7	580	4	US-09-142-078-49
C 10	18	0.7	580	4	US-09-357-141-49
C 11	18	0.7	1124	2	US-08-578-551-1
12	18	0.7	1124	2	US-08-190-982-1
13	18	0.7	1124	4	US-09-408-257-1
14	18	0.7	2149	1	US-08-374-502-1
15	18	0.7	2886	1	US-08-073-383-3
16	18	0.7	2886	3	US-08-328-239A-2
17	18	0.7	2886	5	PCT-US94-06365-3
18	18	0.7	2886	5	PCT-US95-13661-2
19	18	0.7	2890	3	US-08-848-810-1
20	18	0.7	2940	1	US-08-428-415-3
21	18	0.7	2940	1	US-08-379-685-3
22	18	0.7	2940	2	US-08-854-029-3
23	18	0.7	2940	4	US-08-428-762-3
24	18	0.7	3306	1	US-08-261-206A-71
25	18	0.7	7070	1	US-08-619-554-3
C 26	18	0.7	18073	4	US-09-078-294-12
C 27	17	0.6	27	2	US-08-244-122-12

C 28	17	0.6	62	4	US-09-296-607-1	Sequence 1, Appl
C 29	17	0.6	63	2	US-08-776-944-10	Sequence 10, Appl
C 30	17	0.6	66	2	US-08-776-944-11	Sequence 11, Appl
31	17	0.6	188	1	US-08-330-108-2	Sequence 2, Appl
32	17	0.6	188	5	PCT-US92-10087-2	Sequence 2, Appl
C 33	17	0.6	607	4	US-09-328-111-531	Sequence 531, App
34	17	0.6	1223	2	US-08-463-081B-3	Sequence 3, Appl
35	17	0.6	1223	2	US-08-461-379A-3	Sequence 3, Appl
36	17	0.6	1223	2	US-08-462-390B-3	Sequence 3, Appl
37	17	0.6	1223	3	US-08-463-074B-3	Sequence 3, Appl
38	17	0.6	1223	3	US-08-465-585C-3	Sequence 3, Appl
39	17	0.6	1223	3	US-08-652-446-3	Sequence 3, Appl
C 40	17	0.6	1317	3	US-08-915-498B-36	Sequence 36, Appl
41	17	0.6	1662	2	US-08-956-012-2	Sequence 2, Appl
C 42	17	0.6	1668	1	US-08-463-090B-1	Sequence 1, Appl
43	17	0.6	1976	3	US-09-165-042-2	Sequence 2, Appl
44	17	0.6	2009	4	US-09-446-504-17	Sequence 17, Appl
45	17	0.6	2280	2	US-09-055-097-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-568-459A-3
; Sequence 3, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellemis, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568.459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-08-568-459A-3

```

; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5952196e1 Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,058
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607991.8
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmli, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31458-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-844-058-1

Query Match 0.7% Score 19; DB 2; Length 1651;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels

Qy 1253 cttgcaccttacgattcgc 1271
|||||
Db 1171 CTTGCACCTTAGATCTGC 1153

RESULT 4
US-09-422-869-1/c
; Sequence 1, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: GREENAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/422,869
; CURRENT FILING DATE: 1999-10-21
; EARLIER APPLICATION NUMBER: 60/134,175
; EARLIER FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 49136

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; TYPE: DNA
; ORGANISM: Human
US-09-422-869-1

Query Match 0.7%; Score 19; DB 4; Length 49136;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 gcacaggagagaagcaaaag 59
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Db 5275 GCACAGGAGAGCAAAAG 5257

RESULT 5

US-09-142-078-57/C
; Sequence 57, Application US/09142078
; Patent No. 6172041
; GENERAL INFORMATION:
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Zhou, Li-Ming
; APPLICANT: Layer, Richard T.
; TITLE OF INVENTION: Use of Conantokins
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,078
FILING DATE: 10-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US97/12652
FILING DATE: 21-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,377
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/684,750
FILING DATE: 22-JUL-1996

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2314-135.A
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cdna)
ORIGINAL SOURCE:
ORGANISM: Conus lynceus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..282
US-09-142-078-57

Query Match 0.7%; Score 18; DB 4; Length 379;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1764 cagaggatttctgcagga 1781
|||||
Db 139 CAGAGGATTCTGCAGGA 122

RESULT 6

US-09-357-141-57/C
; Sequence 57, Application US/09357141
; Patent No. 6277825
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Layer, Richard T.
; APPLICANT: Zhou, Li-Ming
; TITLE OF INVENTION: Use of Conantokins for Treating Pain
; FILE REFERENCE: 2314-171
; CURRENT APPLICATION NUMBER: US/09/357,141
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 09/283,277
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: US 09/142,078
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: WO US97/12652
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: US 08/762,377
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: US 08/684,750
; PRIOR FILING DATE: 1996-07-22
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Conus lynceus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(282)
US-09-357-141-57

Query Match 0.7%; Score 18; DB 4; Length 379;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1764 cagaggatttctgcagga 1781
|||||
Db 139 CAGAGGATTCTGCAGGA 122

RESULT 7

US-09-142-078-53/C
; Sequence 53, Application US/09142078
; Patent No. 6172041
; GENERAL INFORMATION:
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Zhou, Li-Ming
; APPLICANT: Layer, Richard T.
; TITLE OF INVENTION: Use of Conantokins
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
; STREET: 555 Thirteenth Street, N.W., Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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RESULT      8
US-09-357-141-53/c
; Sequence 53, Application US/09357141
; Patent No. 6277825
;
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Layer, Richard T.
; APPLICANT: Zhou, Li-Ming
;
; TITLE OF INVENTION: Use of Conantokins for Treating Pain
;
; FILE REFERENCE: 2314-171
; CURRENT APPLICATION NUMBER: US/09/357,141
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 09/283,277
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: US 09/142,078
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: WO US97/12652
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: US 08/762,377
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: US 08/684,750
; PRIOR FILING DATE: 1996-07-22
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Conus ochroleucus

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Query Match 0.7%; Score 18; DB 4; Length 580;
Best Local Similarity 100.0%; Pred. No. 51;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1764 cagaggatttctgcagga 1781
|||||

Db 286 CAGAGGATTTCGAGGA 269

RESULT 10

US-09-357-141-49/c
; Sequence 49, Application US/09357141

; Patent No. 6277825

; GENERAL INFORMATION:

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: McCabe, R. Tyler

; APPLICANT: Laver, Richard T.

; APPLICANT: Zhou, Li-Ming

; TITLE OF INVENTION: Use of Conantokins for Treating Pain

; FILE REFERENCE: 2314-171

; CURRENT APPLICATION NUMBER: US/09/357,141

; CURRENT FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: US 09/283,277

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: US 09/142,078

; PRIOR FILING DATE: 1999-02-10

; PRIOR APPLICATION NUMBER: WO US97/12652

; PRIOR FILING DATE: 1997-07-21

; PRIOR APPLICATION NUMBER: US 08/762,377

; PRIOR FILING DATE: 1996-12-06

; PRIOR APPLICATION NUMBER: US 08/684,750

; PRIOR FILING DATE: 1996-07-22

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 49

; LENGTH: 580

; TYPE: DNA

; ORGANISM: Conus radiatus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (127)..(447)

US-09-357-141-49

Query Match 0.7%; Score 18; DB 4; Length 580;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1764 cagaggatttctgcagga 1781
|||||

Db 286 CAGAGGATTTCGAGGA 269

RESULT 11

US-08-578-551-1

; Sequence 1, Application US/08578551

; Patent No. 5854050

; GENERAL INFORMATION:

; APPLICANT: Dalboge, Henrik

; APPLICANT: Christgau, Stephan

; APPLICANT: Andersen, Lene N.

; APPLICANT: Kofod, Lene V.

; APPLICANT: Kauppinen, Sakari M.

; APPLICANT: Nielsen, Jack B.

; APPLICANT: Dammann, Claus

; TITLE OF INVENTION: An Enzyme with Protease Activity

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 58540500 No. 58540500disk of No. 58540500th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10174-6401

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/578,551

; FILING DATE: 01-FEB-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DK 0811/93

; FILING DATE: 06-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO 95/02044

; FILING DATE: 19-JAN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4006.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1124 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Aspergillus aculeatus

US-08-578-551-1

Query Match 0.7%; Score 18; DB 2; Length 1124;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2632 ttgagagagagagagagagag 2649
|||||

Db 1103 TTGAGAGAGAGAGAGAGAG 1120

RESULT 12

US-09-190-982-1

; Sequence 1, Application US/09190982

; Patent No. 5998190

; GENERAL INFORMATION:

; APPLICANT: Dalboge, Henrik

; APPLICANT: Christgau, Stephan

; APPLICANT: Andersen, Lene N.

; APPLICANT: Kofod, Lene V.

; APPLICANT: Kauppinen, Sakari M.

; APPLICANT: Nielsen, Jack B.

; APPLICANT: Dammann, Claus

; TITLE OF INVENTION: An Enzyme with Protease Activity

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 59981900 No. 59981900disk of No. 59981900th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/190,982

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RESULT 14
US-08-374-502-1/c
; Sequence 1, Application US/08374502
; Patent No. 5759805
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew L.
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: CD69 TRANSCRIPTIONAL REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,502
; FILING DATE: 20-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER M.
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22627-20011.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2149 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:

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; NAME/KEY: mat_peptide
; LOCATION: 2080
US-08-374-502-1

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Best Local Similarity 100.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1885 TCACACTGTAGCTTCAA 1868

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; Sequence 3, Application US/08073383
; Patent No. 5443962
; GENERAL INFORMATION:
; APPLICANT: Draetta, Giulio
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; TITLE OF INVENTION: [fillin "Insert Title of Application"]ASSAY AND REAGENTS FOR
; TITLE OF INVENTION: [fillin "ANTI-PROLIFERATIVE AGENTS"]
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,383
; FILING DATE: 19930604
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2886 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1773
US-08-073-383-3

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Db 2863 TTGAGAAAAA 2880

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Job time: 10162 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:28:30 ; Search time 3720.85 seconds
(without alignments)
11744.905 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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36: em_htg_other.*

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4	1084.8	41.3	2641	8	VSNER
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ALIGNMENTS

RESULT 1

PSU67185

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

PSU67185 2650 bp mRNA PLN 06-MAR-1998
Papaver somniferum NADPH:ferrihemoprotein oxidoreductase mRNA,
complete cds.

U67185 GI:2580496

Opium poppy.

Papaver somniferum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Papaver.

1 (bases 1 to 2650)

Rosco,A., Pauli,H.H., Priesner,W. and Kutchan,T.M.

Cloning and heterologous expression of NADPH-cytochrome P450

reductases from the Papaveraceae

Arch. Biochem. Biophys. 348 (2), 369-377 (1997)

98096363

2 (bases 1 to 2650)

AUTHORS Rosco,A. and Kutchan,T.M.
TITLE Direct Submission
JOURNAL Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,
Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany
FEATURES
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/organism="Papaver somniferum"
/db_xref="taxon:3469"
/note="cell suspension culture"
124..2175
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reduces cytochrome c"
/note="cytochrome P-450 reductase"
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BASE COUNT 766 a 514 c 606 g 764 t
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AF302496

LOCUS

DEFINITION

ACCESSION

VERSION

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ORGANISM

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ACCESSION A75959
VERSION A75959.1 GI:6088149
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Kazmaier,M. and Lacroute,F.
METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
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ORSAN (FR); KAZMAIER MICHAEL (FR)
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VERSION     U67186.1 GI:2580498
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Papaveraceae; Eschscholzioidae; Eschscholtzia.
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AUTHORS     Rosco.A., Pauli.H.H., Priesner,W. and Kutchan,T.M.
TITLE       Cloning and heterologous expression of NADPH-cytochrome P450
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JOURNAL     Arch. Biochem. Biophys. 348 (2), 369-377 (1997)
MEDLINE     98096363
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AUTHORS     Pauli.H.H. and Kutchan,T.M.
TITLE       Direct Submission
JOURNAL     Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,
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Qy	2101	atggaatcatctgctgccgaagctgcagtaagaagaactccaagtgaagaacgatattcta	2160
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RESULT	8		
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DEFINITION	Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome	PLN	02-MAR-2001
ACCESSION	P450 oxydoreductase isoform 2 mRNA, complete cds.		
VERSION	AF302497		
KEYWORDS	AF302497.1	GI:13183563	
SOURCE	Populus x generosa		
ORGANISM	Populus x generosa		
	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.		

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Qy 1919 ttattgcctttccacgtgaaggggaaagaagaataatttcaacaataagatgagggaga 1978

Db 2041 TTCCTGCTTCTCGCAGAGGAGCAACCAAGAGATGTGCGAGCACAGATTCAGAGAGA 2100

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Qy 2039 ccaagggaatgccaagatgtccatgcacgttcacatccatttcccaagaacaggagac 2098

Db 2161 CCAAGGGATGCTAGGATGTGCACAGGACACTACATAGTATAGTCCAAAGACAGGAAT 2220

Qy 2099 ccattggaatcattctgctccgaagctgcagtaaaagaactccaagttgaaagaacgatatc 2158

Db 2221 CGTGGATAGCACAGCCGAGAGGCTACAGTGAAGAAATTCAGACAGAGAAGATATT 2280

Qy 2159 taagagatgtctgtgatcgaatgtagcttagcttgccaagtcacctt 2201

Db 2281 TACGAGATGTATGTAATTGACTGAATTTGTTCTTAGGTCAAGTT 2323

RESULT 10

AF302498 2610 bp mRNA PLN 02-MAR-2001

LOCUS Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome

DEFINITION P450 oxydoreductase isoform 3 mRNA, complete cds.

ACCESSION AF302498

VERSION AF302498.1 GI:13183565

KEYWORDS .

SOURCE Populus x generosa.

ORGANISM Populus x generosa.

REFERENCE Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurossids I; Malpighiales; Salicaceae; Populus.

AUTHORS 1 (bases 1 to 2610)

TITLE Functional characterization of cytochrome P450 reductase from the hybrid poplar (Populus trichocarpa x P. deltoides)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2610)

AUTHORS Ro.D.-K. and Douglas,C.

TITLE Direct Submission

JOURNAL Submitted (05-SEP-2000) Botany, University of British Columbia, 6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada

FEATURES Location/Qualifiers

Source 1..2610

/organism="Populus x generosa"

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BASE COUNT 711 a 530 c 631 g 738 t

ORIGIN

Query Match 34.4%; Score 911.2; DB 8; Length 2610;

Best Local Similarity 68.4%; Pred. No. 2e-196;

Matches 1283; Conservative 0; Mismatches 578; Indels 15; Gaps 1;

Qy 323 aagaagagagagattgaagttgatcctcgtgtataaataaagctcaactatatttttggtaactc 382

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Qy 503 aagagaaataaagaagagctcttgggtgtttttcatagtgtagcacttatgtgatggtg 562

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Qy 563 agccaactgacaatgctgcgagattttacaatatggttcaactcaggaacatgaaaggagag 622

Db 629 AGCCTACTGTATAATCGGCAAGGTTCTACAAATGGTTTTACAGAGGGAATAGAGAGGGG 688

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BASE COUNT 709 a 454 c 644 g 749 t
ORIGIN

Query Match 33.0%; Score 875.2; DB 8; Length 2556;
Best Local Similarity 67.9%; Pred. No. 2.9e-188;
Matches 1276; Conservative 0; Mismatches 583; Indels 21; Gaps 3;

Qy	319	aaagaagaagagagattgaagttagctgtaaaattaaagctcaactatatatttttgt 378
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Qy	499	tatgaagaagaataaagaagaagctcttggtgtgttttcaatggttagcaacttatggtag 558
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RESULT 14
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DEFINITION Sequence 3 from Patent WO9321326.
ACCESSION A75961
VERSION A75961.1 GI:6088151
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2423)
Kazmaier,M. and Lacroite,F.
METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES
Patent: WO 9321326-A 3 28-OCT-1993;
ORSAN (FR); KAZMAIER MICHAEL (FR)

FEATURES
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2267. .2423
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BASE COUNT
ORIGIN

Query Match 33.0%; Score 875; DB 6; Length 2423;
Best Local Similarity 66.5%; Pred. No. 3.2e-186;
Matches 1326; Conservative 0; Mismatches 60; Indels 27; Gaps 4;
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Qy 1748 cagggtagctcctcctcagagagattcttcgaggaagaagaatggccctcaggaataatgggtg 1807
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Db 2262 TATGGTAACGAAA 2274

RESULT 15
LOCUS AF024634 2466 bp mRNA PLN 26-JAN-1998
DEFINITION Petroselinum crispum NADPH cytochrome P450 reductase (CPR2) mRNA,
complete cds.
ACCESSION AF024634
VERSION AF024634.1 GI:2809384
KEYWORDS
SOURCE parsley.
ORGANISM Petroselinum crispum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
REFERENCE 1 (bases 1 to 2466)
AUTHORS Koopmann,E. and Hahlbrock,K.
TITLE Differentially regulated NADPH:cytochrome P450 oxidoreductases in
parsley
Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14954-14959 (1997)
JOURNAL 2 (bases 1 to 2466)
MEDLINE 98070859
REFERENCE Koopmann,E. and Hahlbrock,K.
AUTHORS Direct Submission
TITLE Submitted (12-SEP-1997) Biochemistry, Max-Planck-Institut fuer
JOURNAL zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln 50829, Germany
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ISEGAYIYVCGDARKMARDVIRMLHTIAQSQGALDSSKABESWKNLQMGRLYLRDVM"
BASE COUNT 660 a 474 c 617 g 715 t
ORIGIN

Query Match 33.08; Score 874; DB 8; Length 2466;
Best Local Similarity 66.38; Pred. No. 5.5e-188;
Matches 1296; Conservative 0; Mismatches 640; Indels 18; Gaps 2;

Qy	286	aaacatattgaacattataaaccataattgataaagaagaagagagattgaattgat	345
Db	220	AAATCAGTTGACCCGCCCAAGCTGATTACCGAAAGTTGAAATTGAAGATGAAGTTGAT	279
Qy	346	cctggtaaaataaagctcacatattttttgtaactagactggtaactgctgaaggattt	405
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Qy	406	gctaaggcattggcagaagaataaaggcaaaagtacaagaagaagcattggttaaagtagtt	465
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Qy	466	gacctggatgactatgcagcggagatgatcaatatgaagagaataaagaagaagctct	525
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Qy	826	cagttgtcacaagatgaggatgctgctcttcagtggtcacacagctatatgtactactgt	885
Db	760	AAGTTGCTTTTGGATGAGGA--TGACACATCTGCTGCAACTCCTTTACACAGCTGCTGTT	816
Qy	886	cctgaatacagggtagtgattcaagaaactacggtcgcggtcttggaatgaataacacata	945
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Db	997	ATTTCCACACACGGGCTTTCATATGAACCTGCTGACCACGTCGGGGTCTACTGTGAGAAT	1056
Qy	1126	tgcatgaactgttcgagaagcagggaagcgtgtgtggtcacaacccctggatttgcgtttt	1185
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Qy	1186	tcaattcacaggataaagaagaacgggttcaccccgagggaagctcattaccacctctcttc	1245
Db	1117	TCTGTCCATATTGACGCGAAGATGSAACACACACTTACTTGGAGGCTCTCTGCGCACCTCCC	1176
Qy	1246	ccaggtccttncaccttaagcatctgcccctagcacgctatgctgatatcttttgaaatcctct	1305
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Qy	2011	gacggttatctctatgtgtgtggtgaatccaaagggaatggccagagatgctccatcgacg	2070
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Db	2017	CTTCACAAATTCACAGGAGCAGGAGCTCTTGACAGCAGCAAGCGGAGAGCTGGGTT	2076
Qy	2131	aagaactcctaagtttgaagaacgatatcctaagagatgtctggtgatcgaatgtagcttgc	2190
Db	2077	AAGAACCCTTCAATGACTGGGAGGTATCTTCGTGATGTATGTAATTTGTTCTTCCAGTGC	2136
Qy	2191	caagtcctcccttttctggctggctgttatttggt	2224
Db	2137	AGCCGACCTTGGTTATGTAGATAAGTTTATGAT	2170

Search completed: December 27, 2001, 14:12:13
Job time: 6223 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:28:30 ; Search time 224.31 Seconds
(without alignments)
10124.625 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaaaaaaaaaa 2649

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2645.8	99.9	2650	AA08517	Poppy cytochrome P
2	983.4	37.1	2114	AA051236	Plant NADPH cytoch
3	958.6	36.2	2558	AA08520	Poppy cytochrome P
4	895.4	33.8	2136	AA044709	Arabidopsis thalia
5	875	33.0	2423	AA051237	Plant NADPH cytoch
6	859.8	32.5	2112	AA051238	Plant NADPH cytoch
7	231.8	8.8	485	AA035800	Zea mays DNA fragm
8	192.8	7.3	1872	AA065716	Oxidoreductase gen
9	192.8	7.3	3435	AA081743	Plasmid pAMP19.
10	192.8	7.3	3453	AA081746	Plasmid pALP25.
11	191.4	7.2	3399	AA081747	Plasmid pALP4. A

12	191.2	7.2	2037	8	AA070925	Sequence encoding
13	191.2	7.2	3453	9	AA081744	Plasmid pALP1. A
14	187.6	7.1	2450	8	AA070605	Plasmid pRF1 encod
15	170.4	6.4	3489	9	AA081745	Plasmid pALP17.
16	169.4	6.4	3310	21	AA029331	Partial sequence o
17	169.4	6.4	3311	21	AA0293079	Partial sequence o
18	167.4	6.3	8475	22	AA076964	Genetic construct
19	167.4	6.3	8492	22	AA076963	Genetic construct
20	167.4	6.3	8537	22	AA076962	Genetic construct
21	167.2	6.3	1872	9	AA081748	Plasmid pAXP2. A
22	165.4	6.2	2034	22	AA076960	Human derived cyto
23	165.4	6.2	2034	22	AA076961	Human derived cyto
24	162.4	6.1	2403	20	AA0219778	Human P450 reducta
25	162.4	6.1	2403	20	AA0207749	Human P450 reducta
26	159	6.0	1851	20	AA0219779	Human anchorless P
27	159	6.0	1851	20	AA0207750	Human P450 reducta
28	155.6	5.9	2049	22	AA026033	DNA encoding rabbl
29	114	4.3	936	22	AA058252	Oligonucleotide D1
30	114	4.3	936	22	AA058254	Oligonucleotide D1
31	114	4.3	936	22	AA058257	Oligonucleotide D1
32	114	4.3	936	22	AA058259	Oligonucleotide D2
33	114	4.3	936	22	AA058262	Oligonucleotide D2
34	114	4.3	938	22	AA058255	Oligonucleotide D1
35	112.6	4.3	936	22	AA058252	Oligonucleotide D1
36	112.6	4.3	936	22	AA058254	Oligonucleotide D1
37	112.6	4.3	936	22	AA058257	Oligonucleotide D1
38	112.6	4.3	936	22	AA058259	Oligonucleotide D2
39	112.6	4.3	936	22	AA058262	Oligonucleotide D2
40	112.6	4.3	938	22	AA058255	Oligonucleotide D1
41	111.8	4.2	4145	21	AAA30567	Oligonucleotide D1
42	108	4.1	4206	21	AAA30566	Genomic DNA encodi
43	102.8	3.9	3155	22	AA054060	S. epidermidis gen
44	102.8	3.9	4055	22	AA053993	S. epidermidis gen
45	99.6	3.8	4151	20	AA023663	B. bassiana POPs r

ALIGNMENTS

RESULT 1
AA08517
ID AA08517 standard; DNA; 2650 BP.
AC AA08517;
AC AA08517;
DF 19-JUL-1999 (first entry)
DF Poppy cytochrome P450 reductase.
DE Opium poppy; alkaloids; cytochrome P450 reductase; morphine;
KW codeine; oripavine; thebaine; transformation; crop yield; probe;
KW primer; ss.
XX Papaver somniferum.
XX
XX Key Location/Qualifiers
XX CDS 124..2175
XX FT /*tag= a
XX FT /product= "Cytochrome P450 reductase"
XX
XX W09911765-A1.
XX
XX PD 11-MAR-1999.
XX
XX PF 28-AUG-1998; 98WO-AU00705.
XX
XX PR 29-AUG-1997; 97AU-0008872.
XX
XX PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
XX PI Atkins DG, Fist AJ, Kutchan TM, Zenk MH;
XX
XX WPI; 1999-214703/18.

DR P-PSDB; AAW85680, AAW85682.
XX Nucleic acid encoding cytochrome P-450 reductase from poppy
XX
XX PS Claim 3; Fig 9a; 58pp; English.
XX
XX Transforming plants with a nucleic acid molecule encoding cytochrome
CC P450 reductase alters the yield and/or type of alkaloids produced.
CC In opium poppies it specifically increases the yield of medically
CC useful alkaloids such as morphine, codeine, oripavine and thebaine.
CC Sequences complementary to the coding sequence of cytochrome P450
CC reductase are useful as probes, primers and antisense sequences, or
CC for design of ribozymes. Transformation with DNA encoding the
CC cytochrome P450 reductase allows regulation of the total alkaloid
CC content and of the relative proportions of individual alkaloids.
CC produced. Increasing the alkaloid content of poppy straw should
CC reduce the cost of alkaloid production. Cytochrome P450 reductase
CC is the rate-limiting enzyme in biosynthesis of alkaloids in poppies.
CC Peptide fragments of the cytochrome P450 reductase are described in
CC AAW85672-W85678.
XX
SQ Sequence 2650 BP; 766 A; 514 C; 606 G; 764 T; 0 other;

Query Match 99.9%; Score 2645.8; DB 20; Length 2650;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2647; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 61 cgaattcacttgaaatacattcgattgtctctctctgttttaagcttcagctctcgta 120
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DT 11-MAY-1994 (first entry)
XX XX
DE DE
XX XX
XX Plant NADPH cytochrome P450 reductase (ara B).
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XX
XX (ORSA-) ORSAN.
XX
XX Kazmaier M, Lacroute F, Mignotte-vieux C, Minet M;
XX Pompon D;
XX
XX WPI: 1993-351736/44.
XX
XX P-PSDB; AAR43581.
XX
XX New DNA encoding plant NADPH cytochrome P450 reductase - cloned
XX by functional complementation in yeast, also recombinant enzyme
XX useful in P450 mediated bioconversion processes
XX
XX Claim 11; Figure 9; 79pp; French.
XX
XX A new method for determining whether a DNA sequence encodes an NADPH
XX cytochrome P450 reductase involves transforming yeasts with plasmids
XX of a total cDNA bank of plant(s). The yeasts used in the procedure
XX are incapable of producing their own NADPH cytochrome P450
XX reductase. They are then exposed to a cytochrome P450 inhibitor at a
XX level which is lethal to the yeast cells but not to cells which,
XX because of the transformation, now contain an active NADPH
XX cytochrome P450 reductase. Surviving clones are then isolated and
XX plasmid DNA extracted. The gene is inserted into the plasmid at a
XX site which places it under the control of an inducible promoter.
XX
XX Sequence 2114 BP; 603 A; 400 C; 542 G; 569 T; 0 other;
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Query Match 37.1%; Score 983.4; DB 14; Length 2114;
Best Local Similarity 71.1%; Pred. No. 3e-254;
Matches 1337; Conservative 0; Mismatches 526; Indels 18; Gaps 2;

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Qy 266 aatcttctgtcttctcaatcaaaaacaccttattgaacctataaaccaataattgataaagaag 325
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RESULT 5
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 ID AAQ51237 standard; cDNA; 2423 BP.
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 AC AAQ51237;
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 DT 11-MAY-1994 (first entry)
 XX
 DE Plant NADPH cytochrome P450 reductase (ara C).
 XX
 KW NADPH cytochrome P450 reductase; functional complementation;
 XX identification; ss.
 OS Arabidopsis thaliana.
 XX

PH Key Location/Qualifiers
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 FT misc_difference 410..412
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 FT misc_difference 881..883
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 FT misc_difference 1637..1639
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 FT misc_difference 1763..1765
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 FT /transl_except= AGA encodes Lys.
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 FT WO9321326-A.
 FT 28-OCT-1993.
 FT 13-APR-1993; 93WO-FR00367.
 FT 13-APR-1992; 92FR-0004491.
 FT (ORSA-) ORSAN.
 FT Kazmaier M, Lacroute F, Mignotte-vieux C, Minet M;
 FT Pompon D;
 FT WPI; 1993-351736/44.
 FT P-PSDB; AAR43582.
 FT New DNA encoding plant NADPH cytochrome P450 reductase - cloned
 FT by functional complementation in yeast, also recombinant enzyme
 FT useful in P450 mediated bioconversion processes
 FT Claim 11; Figure 10; 79pp; French.
 FT A new method for determining whether a DNA sequence encodes an NADPH
 FT cytochrome P450 reductase involves transforming yeasts with plasmids
 FT of a total cDNA bank of plant(s). The yeasts used in the procedure
 FT are incapable of producing their own NADPH cytochrome P450
 FT reductase. They are then exposed to a cytochrome P450 inhibitor at a
 FT level which is lethal to the yeast cells but not to cells which,
 FT because of the transformation, now contain an active NADPH
 FT cytochrome P450 reductase. Surviving clones are then isolated and
 FT plasmid DNA extracted. The gene is inserted into the plasmid at a
 FT site which places it under the control of an inducible promoter.
 FT SQ Sequence 2423 BP; 674 A; 497 C; 552 G; 700 T; 0 other;

Query Match 33.0%; Score 875; DB 14; Length 2423;
 Best Local Similarity 66.5%; Pred. NO. 4.5e-225;
 Matches 1326; Conservative 0; Mismatches 640; Indels 27; Gaps 4;


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DE Plant NADPH cytochrome P450 reductase.
XX
KW NADPH cytochrome P450 reductase; functional complementation;
KW identification; ss.
XX
OS Heliantus tuberosus.
XX
FH Key Location/Qualifiers
FT CDS 1..2016
FT     /product= NADPH cytochrome P450 reductase.
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FT     /transl_except= AGA encodes Lys.
FT misc_difference 157..159
FT     /tag= c
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FT misc_difference 418..420
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FT misc_difference 817..819
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PN
XX
XX 28-OCT-1993.
XX
XX 13-APR-1993; 93WO-FR00367.
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XX 13-APR-1992; 92FR-0004491.
XX
XX (ORSA-) ORSAN.
XX
XX Kazmaier M, Lacroute F, Mignotte-vieux C, Minet M;
PI Pompon D;
PI
XX
XX WPI; 1993-351736/44.
DR
XX P-PSDB; AAR43583.
XX
XX New DNA encoding plant NADPH cytochrome P450 reductase - cloned
PT by functional complementation in yeast, also recombinant enzyme
PT useful in p450 mediated bioconversion processes
XX
XX Claim 11; Figure 11; 79pp; French.
XX
XX A new method for determining whether a DNA sequence encodes an NADPH
CC cytochrome P450 reductase involves transforming yeasts with plasmids
CC of a total cDNA bank of plant(s). The yeasts used in the procedure
CC are incapable of producing their own NADPH cytochrome P450
CC reductase. They are then exposed to a cytochrome P450 inhibitor at a
CC level which is lethal to the yeast cells but not to cells which,
CC because of the transformation, now contain an active NADPH
CC cytochrome P450 reductase. Surviving clones are then isolated and
CC plasmid DNA extracted. The gene is inserted into the plasmid at a
CC site which places it under the control of an inducible promoter.
XX
XX Sequence 2112 BP; 591 A; 422 C; 506 G; 593 T; 0 Other;
SQ

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Query Match 32.5%; Score 859.8; DB 14; Length 2112;
 Best Local Similarity 67.6%; Pred. No. 5,2e-221;
 Matches 1263; Conservative 0; Mismatches 582; Indels 24; Gaps 3;

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Db 221 ctggaaccgctgaagggtttctgaaggcgttttgaagaagcgaagcgcatatgaaa 280
Qy 446 aagcagttgttaaaagttagttgacctggatgactatgcagccgagatgatcaatgaag 505
Db 281 aagcgtgttttaaaagttgattgattggatgattatgctgctgctgatgaggagatgcag 340
Qy 506 agaaattaaagaagagctcttgggtgttttttcattaggtagccacttatggtggtgagc 565
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Qy 566 caactgacaatgctgcgagattttcaaatggttctcaactcaggaacatgaaaggagagt 625
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Db 2012 ggtgatcta 2020

RESULT 7
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KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX Zea mays subsp. mays.
XX EP1033405-A2.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
PF 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.

PR	28-APR-1999;	99US-0131449.	PR	21-JUL-1999;	99US-0144814.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.
PR	30-APR-1999;	99US-0132407.	PR	21-JUL-1999;	99US-0145088.
PR	04-MAY-1999;	99US-0132484.	PR	22-JUL-1999;	99US-0145085.
PR	05-MAY-1999;	99US-0132485.	PR	22-JUL-1999;	99US-0145087.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145089.
PR	06-MAY-1999;	99US-0132487.	PR	22-JUL-1999;	99US-0145192.
PR	07-MAY-1999;	99US-0132863.	PR	23-JUL-1999;	99US-0145145.
PR	11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145218.
PR	14-MAY-1999;	99US-0134218.	PR	23-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134219.	PR	26-JUL-1999;	99US-0145276.
PR	14-MAY-1999;	99US-0134221.	PR	27-JUL-1999;	99US-0145913.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145918.
PR	18-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-0145919.
PR	19-MAY-1999;	99US-0134941.	PR	28-JUL-1999;	99US-0145951.
PR	20-MAY-1999;	99US-0135124.	PR	02-AUG-1999;	99US-0146386.
PR	21-MAY-1999;	99US-0135353.	PR	02-AUG-1999;	99US-0146388.
PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146389.
PR	25-MAY-1999;	99US-0136021.	PR	03-AUG-1999;	99US-0147038.
PR	27-MAY-1999;	99US-0136392.	PR	04-AUG-1999;	99US-0147204.
PR	28-MAY-1999;	99US-0136782.	PR	04-AUG-1999;	99US-0147302.
PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	23-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139461.	PR	25-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	30-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	19-JUL-1999;	99US-0144325.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144331.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144334.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159329.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159637.
PR			PR	14-OCT-1999;	99US-0159638.

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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      8.8%; Score 231.8; DB 21; Length 485;
Best Local Similarity 70.2%; Pred. No. 2e-52;
Matches 339; Conservative 0; Mismatches 142; Indels 2; Gaps 2;

QY 1694 acttcaaggttacagctgacccctcaactcaactcaattatcatgtgtggacctgtacaggt 1753
Db 1 attcaagttacctgtcatcgtccctccactcatcatcatgtgtgtggtggacaggt 60

QY 1754 tagctccttcagaggattctgcaggaaagaatggccctcaaggaaatggtgtccaac 1813
Db 61 g-ctccttttagaggctctctgcaggaaagggttagcattgaaacaatctgggcagaat 119

QY 1814 ttggocccagcagtgctcttttttgcgatgtaggaatcgttaataatggaacttatttgaag 1873
Db 120 tgggcacttcaatcctttcttttggatgcaggaaocgtaatatggactacatatgaag 179

QY 1874 acgaactaaacaactctgcggacagaggagtcattctggagctagttatgcttttcaac 1933
Db 180 atgagtgcacaactttctctggaggggggcgctcttctgagctaatgtgtcatctctc 239

QY 1934 gtgaaggggaaagaaggaataatgttcaacataagaatgatggagaaacgacgagtgtat 1993
Db 240 ggaaggggccaaagaagaataatgtgcagcataagaatgtggaaaaggccacagaaattt 299

QY 1994 ggaatgtgatacaggggacggttattctctatgtgtgtgtgatgccaaagggaatggcca 2053
Db 300 ggaacatcatcctcaaatggtgttacttataatgtttgcgtgtatgccaaagggaatggcta 359

QY 2054 gagatgtccatcgacgttgcataccattgccaaagacagaggaccatgggaatcatctg 2113
Db 360 ggaatgtcacacaaatgctctacataaatatgtccaaagacagaggatctttggataactcca 419

QY 2114 ctggcga-agctgcagtaagaactccaaagttggaagacgatatctaaagagatgtctgg 2172
Db 420 aaaccgagagctatgtaaaaaagcctgcgagatgggaagggaaggtaacctcgtgatgtatgg 479

QY 2173 tga 2175
Db 480 tga 482
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RESULT 8

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AAQ65716
ID AAQ65716 standard; DNA; 1872 bp.
XX
XX
XX AAQ65716;
XX
XX
DT 18-JAN-1995 (first entry)
XX
XX Oxidoreductase gene.
XX
XX Oxidoreductase; monooxygenase activity; cytochrome C; reductase activity;
```

```
KW NADPH-cytochrome P-450; polyfunctional; rat; liver; ds.
XX
XX Synthetic.
XX JP06113836-A.
XX
XX 26-APR-1994.
XX
XX 25-OCT-1991; 91JP-0305592.
XX
XX 25-OCT-1991; 91JP-0305592.
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
XX
XX WPI; 1994-172734/21.
XX
XX New oxidoreductase having NADPH-cytochrome P-450 reductase and
PT cytochrome-P-450 monooxygenase activity - produced by yeast cells
PT transformed with chimeric gene
XX
XX Claim 2; Page 7; 8pp; Japanese.
XX
XX This sequence represents the coding sequence of an oxidoreductase
CC which has both the monooxygenase activity of cytochrome C and the
CC reductase activity of NADPH-cytochrome P-450. The encoded reductase
CC is a polyfunctional enzyme containing fragments of two rat liver
CC genes.
XX
XX Sequence 1872 BP; 439 A; 527 C; 544 G; 362 T; 0 other;
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```
Query Match      7.3%; Score 192.8; DB 15; Length 1872;
Best Local Similarity 49.0%; Pred. No. 1.2e-41;
Matches 908; Conservative 0; Mismatches 872; Indels 72; Gaps 12;

QY 354 aattaagctcactatatttttggctactcagactgtactgtcgaaggatttgcctaagc 413
Db 66 aaggaaacattatcgattatctatgtctccagacgggaacccgtgagagatttgcacaacg 125

QY 414 attgacagaagaataatgaaggcaagtacagaagaacagctgtttaaagtatgtgacctga 473
Db 126 gctgtccaaggatgccaccgctacgggatgcgggcatgtccgcagaccctgaagagta 185

QY 474 tgaactatgcagccgagatgatcaatatgaagaaaaattaaagaaagatcttctgtgt 533
Db 186 tgacttggccgacctgagcagcctgctctga-----gatcgacaagtccctggtagt 236

QY 534 ttctatggttagccacttatggtgatggtgagccaaactgacaatgctgcgagattttacaa 593
Db 237 ctctcgatggccacatacgcgagaggcgacccacggacaatgcgcaggaacttctatga 296

QY 594 atggttcactcagggaacatgaaaggggagagtgccttcagcaactaaactataggtgttt 653
Db 297 ctggctg-----caggagactgacgtgacacctcactgggttcaagtgttgcgtatt 347

QY 654 tggtttgggtaacctcaatacagacatttcaacaagatcgcggtagatgtgtagagaca 713
Db 348 tggcttgggaacaagacctatgacacctcaatgccatgggcaaglatgtagcacgcg 407

QY 714 actcgttaacaaggttgcaagcgcattgttcaagtggggcgctcggtgacgatgataatg 773
Db 408 gctggagcagcttggcgccagcgcattctttagttggcccttggtagatgacgagggaa 467

QY 774 catgaagatgatttactgcttggcgagaattgttggactgaattggatcagttgct 833
Db 468 ctgggaagaggatttcatcactgcgtggaggagcagttctgtgccagctgtgtgcgagttct 527

QY 834 caaagatgaggtgctgctccttcagtgactacaccgtatatattgctacttctccgaata 893
Db 528 -----tggggtagaagccactggggagagtcgagcattcgcagcaglatgagctogt 581

QY 894 cagggtagtgattcacgaaactacgt-----cgggctctggtgataaaacacataaac 950
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Db 582 ccacgaagacatggaacgtagccaaggtgtacacgggtgagatggtggtcgtctgaagagcta 641
Qy 951 tgcataacggcgatgttgcaatttgatattccatcccttcgacgaacattgttgcctcaaca 1010
Db 642 cgagaaccaaacccttcgtatgctaagaatccattcccttggtgctgcacgcgcaa 701
Qy 1011 agagagatcccaaaaacccaagctgatagataccttgatatacattctggagttgcagatc 1070
Db 702 ccggaagctgaaccaaggca---ctgagcggcatctaatgcacctggagttggacatctc 758
Qy 1071 aggcctctcccttacatatgaactggagatcatgttggtgtttatgctgagaaactgga 1130
Db 759 agactccaagaacaggtatgaactggagatcacgtggtgtgtacccagccaatgaactc 818
Qy 1131 tgaacctgtcagggaagcaggagctgttggttcaacccctggattgtgttttcaat 1190
Db 819 agccctggtcaaccagattggggagatcctggagctgaactggatgtcatcatgtctct 878
Qy 1191 tcacacggataaagaacgggtgcacccacgggaagctcatattaccacctctcttcccagg 1250
Db 879 aaaca---atctcgatgagagtgcaacaag-----aagcatccgttccctcg 923
Qy 1251 tccctgacattacgatctgcccagcagcgtatgctgatacttttgaatccctctagaaa' 1310
Db 924 ccccaacctaccgcacggccctcaactactacctgacatcactaacccgcacgcac 983
Qy 1311 ggtctctctgattgctgtccgtcatgcatctgtacccagtgacagcagagatgctg 1370
Db 984 caatgtctctacgaactggcaagtagccttcagagccctcgaggcaggagcaactgca 1043
Qy 1371 ctttttg-----tcatcacctctgggaagaatgagtattcaaaatgggtagtgggaag 1424
Db 1044 caagatggcgctcatctcagcggcagggaagcagagctgtacctgagctgggtggtgaagc 1103
Qy 1425 tcagaggagctcttggagatcatggccgagtttccatcagcaaaaacccctcttgggt 1484
Db 1104 ccggaggacacatccttagccatcctcaagactaccatccactgctggcgccacct---cga 1160
Qy 1485 gtctttgctgagtagccctcgcttaccgctcgatactattctatctcatctctcc 1544
Db 1161 ccactgtgtgagctgtgcacgcctcagggcccgatctactactcattgcccctatcctc 1220
Qy 1545 taagttgtcctccaaatcatgtgacgtgtgctttagtatatggttcaaaagccctac 1604
Db 1221 caaggtccaccccaactcctgtcacatctgtgcctggcgtggagtagcaagcgaagtc 1280
Qy 1605 cggaaaggttcaaccgagagtggttgcacatggat-----gaagcatgcagttccctca 1658
Db 1281 tggcggagtgaacaagggttggccactagctggtgcttcgggccaaggaaaccagcaggga 1340
Qy 1659 ggatagctg-----ggctcctatttttggttcgaacgtcaaaacttcaagtaccagc 1709
Db 1341 gaatggcgccgccccttgggtaccatgttgcgtgcgaaaactcagttccgcttgccttt 1400
Qy 1710 tgacccctcaactccaattatcatggtggacctggttacagggttagctctcttcagagg 1769
Db 1401 caagtcaccacacactctcatcatgtgtggcccgccagctgggattgcccctttcatggg 1460
Qy 1770 atttctcaggaagaatagggccctcaagaaatggtgctcaacttggcccgagctgct 1829
Db 1461 cttcatccaggaacagcttggcttcgagagcaaggcaggaggttgggagagacgtgct 1520
Qy 1830 ctttttccgattaggaatcgtataataggaacttattatgaagacgaactaaacaactt 1889
Db 1521 atactatggctgcgcgcctcggatgaggaactatctgtaccgtgaagagctagccgctt 1580
Qy 1890 cgtggaacgagaggtcattctcggagctagttattgctcttttccagctgaagggaagaa 1949
Db 1581 ccacaaggacggtgcccctcaacgcgccttaatgtgccccttttcccggggagcaggccaca 1640
Qy 1950 ggaatatgtcaacataaagatgaggaagaagcaacgagatgtatgggaatgtgatcagg 2009
Db 1641 ggtctatgtccagcaccttctgaagagagacagagggaacacactgttggaaagctgataccaga 1700

Qy 2010 ggaacggt---tatctctatgtgtgtggtgaccccaagggaatggccagagatgtccatcg 2066
Db 1701 gggcggtgcccacatctatgtgtgcgggagtgctcgaataatggccaaagatgtgcaaaa 1760
Qy 2067 cactgtgcataccattgcccaagaacaggagcccatggaatcatctgtgcgaagctgc 2126
Db 1761 cacattctatgacattgtggtgagttcgggcccattggagcacaccaggtctggaacta 1820
Qy 2127 agtaagaagaactccaagtgtgaagaacgatatacttaagagatgtctgtgctgacg 2178
Db 1821 tgttaagaagctgtagcaaacgggcccgtactactactagatgtgtgagctag 1872

RESULT 9
ID AAN81743 standard; DNA; 3435 BP.
XX
AC AAN81743;
XX
DT 19-OCT-1990 (first entry)
XX
DE Plasmid pAMP19.
XX
KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
KW industrial waste; ss.
XX
FH Key Location/Qualifiers
FT CDS 1..3435
FT /*tag= a
XX
PN JP63044888-A.
XX
PD 25-FEB-1988.
XX
PF 12-AUG-1986; 86JP-0187713.
XX
PR 12-AUG-1986; 86JP-0187713.
XX
PA (AGEN) AGENCY OF IND SCI TECH.
XX
DR WPI; 1988-094816/14.
DR P-PSDB; AAP81334.
XX
PT Chimera fusion enzyme' gene - coding oxidation enzyme of cytochrome p-450
PT and NADPH-cytochrome p-450 reduction enzyme
XX
PS Disclosure: ; p; Japanese.
XX
CC This plasmid is used in the prodn. of a chimeric fusion enzyme
CC comprising the genes for the oxidation enzyme of cytochm. p-450 and the
CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochm. p-450
CC reduction enzyme. See also AAN81744-48.
XX
SQ Sequence 3435 BP; 816 A; 945 C; 940 G; 734 T; 0 other;

Query Match 7.3%; Score 192.8; DB 9; Length 3435;
Best Local Similarity 49.0%; Pred. NO. 1.6e-41;
Matches 908; Conservative 0; Mismatches 872; Indels 72; Gaps 12;

Qy 354 aattaagctactatatttttgggtactcagactggttactgctgaaggatttgcataaggc 413
Db 1629 aaggaaacttatctgtattctatggtctccagacgggaacccgtgaggagtttgcacacc 1688
Qy 414 attggcagaagaataaaggcaaaagcagcagttgttaaaagttagttgacctgga 473
Db 1689 gctgtccaaagatccccaccctcagcggatcggggcatgtcccagacacctggaagagta 1748
Qy 474 tgactatgaccccgaggatgatcatataagagaaaataaagaaagagctcttgggtgtt 533
Db 1749 tgaactggccgacctgagcagccctgcctga-----gacgcagaagtcctcgtgtagt 1799

QY 534 ttctcgttagccacttatgttgtagccaaactgacaatgctgcgagattttcaaa 593
 Db 1800 cttctgcattgccacatacagagagggcgaccccgagacaatgcgaggactcttatga 1859
 QY 594 atggttcaactcaggaaactgaaagggagtggtggttcagcaactaaattatgtgtttt 653
 Db 1860 ctggctg-----caggagactgacgtggacctcactcgggtcaagtgttgcgtatt 1910
 QY 654 tggtttgggtaacctcaatcacgacgacatttcaacaagatccggttagatgtagtagca 713
 Db 1911 tggcttgggaacagacctatgacaactcaatgccctggcaagtgtggaccagcg 1970
 QY 714 actcgttaaacaggtgcgaagcgatgttcaagtgggctcggctgacgatgatcaatg 773
 Db 1971 gctgagacgctggcgccacgcgactcttgagttggccttggctgtagatgacgggaa 2030
 QY 774 catgaagatgattttaactgcttgcggagaaattgttggactgaattggatcagttgct 833
 Db 2031 cttggaagaggtttcacaactcagtgaggagcagttcttggccagctgtgtgcgagttct 2090
 QY 834 caaagatgagatgctgctctcactgaggtacacccgtatatgtactgttctcgaata 893
 Db 2091 -----tggggtagaagccactgggagagtgctgagcattcgccagtgatgagctcgtggt 2144
 QY 894 cagggtagtgattcacgaaactacggt---cgcggtcctggatgataaacacataaatac 950
 Db 2145 ccacgaagacatgagcgttagccaaggtgtacacgggtgagatggcgctctggaagacta 2204
 QY 951 tgcatacggcgtggttgatttgatttccatctctccactcttgcgaacattgtttgctcaaca 1010
 Db 2205 cgagaaccagaaacccctctcgatgctaagaatccattcctcgtgctgtccaccgcca 2264
 QY 1011 aagagagctccacaacccaagctcgtatagatccctgtatacatctggaggttcgaacatc 1070
 Db 2265 ccggaaactgaaccagca---ctgagcggcatctaatacctcggatggatggacatctc 2321
 QY 1071 aggcctctcccttacatgatgagactggagatcatgttggtgttatgctgagaaactgcga 1130
 Db 2322 agactccaagatcaagttatgaatctggagatcacgttgctgtgtaccacgccaatgaetc 2381
 QY 1131 tgaactctcagggaagcagggaagctgttgggtcaacccctcggattgctgttttcaat 1190
 Db 2382 agccttggtcaaccagattgggagatcctggagctcgtgacctggatgctcactatgctct 2441
 QY 1191 tcacagataaagagacggttcccccagggaagctcattacccactcctttcccagg 1250
 Db 2442 aaaca---atctcgatgaggagtcgaacaag-----aagcatccggttccctcg 2486
 QY 1251 tccctgcaccttaecatctgccttagcacgctatgctgatcttttgaatcctcctagaaa 1310
 Db 2487 cccacacctaccgcagcgccctcaactactactactcctgacatcactaaccgcacgac 2546
 QY 1311 ggcctctctgattgctctgcgctcactgcatctgtacccagtgaaagcagagagattgcg 1370
 Db 2547 caatgctctacgaactcggcagcagtagcctcagagcctcggagcaggagcaactgca 2606
 QY 1371 ctttttg-----tcatacctcttggaagaatgagtatitcaaaatgggtagttgggaag 1424
 Db 2607 caagatggcgtcatcctcagcgagggcaagagagctgacactgagctgggtgggaagc 2666
 QY 1425 tcagaggagcttttggagatcatggcgagtttccatcagcaaaacccctcttgggtgt 1484
 Db 2667 ccggaggcacatccttagcactcctcgaactcactcactcactcactcactcactcactc 2723
 QY 1485 gtcttctgctcagtagccctcgtctaccgctcctcgatactattctatctcactcctccc 1544
 Db 2724 ccacctgtgtgagctgtgcacgcgctcaggcccgatactactcacttgcctcactcctc 2783
 QY 1545 taagtgttctcctcaagaattctgtagcgtgtgtcttttagtatatggtcaagcccttac 1604
 Db 2784 caaggtccaccccaactccgtgcacatctgtcgcggcggtggagtagcagaagcagctc 2843
 QY 1605 cggaaaggttcaccgagaggtgtgttcgacatggat-----gaagcatgtagttctctca 1658

Db 2844 tggcgcgtgaacaagggggtggccactagctlggcttcgggccaaaggaaaccagcaggcga 2903
 QY 1659 ggatagctg-----ggctcctatttttgcgaacgctcaaaacttcaaagtaccagc 1709
 Db 2904 gaatggcgcgcgccctgggtaccatgttctgtgcgcaaatctcagttccggttgccttt 2963
 QY 1710 tgacctcactcaactcaatataatgtagtgaggacctgtgacagggttagctcctctcagagg 1769
 Db 2964 caagtccaccacacgtctcatcattggtggccccggcactggattgcccccttcatggg 3023
 QY 1770 atttctgcaggaagaatggccccccaaggaataatggttgcctaaacttggccccagcgtgct 1829
 Db 3024 ctctcatcaggaacagacttggcttcgagagacaaggaaggtgggagagacgtcgtc 3083
 QY 1830 ctttttcggatgtaggaatcgtaatatgtaacttctattatgaagcgaactaaacaatt 1889
 Db 3084 atactatggctgcggcgtcgtgagtaggactatctgtaccgtgaagagtagccgctt 3143
 QY 1890 cgtggaacgaggagtcatttcggagactagtatttcccttttcaactgtaaggggaaaaagaa 1949
 Db 3144 ccacaagacggtgccccccaacgcagcttaattgtgcccctttccccgggagcagcccccaa 3203
 QY 1950 ggaatatgttcaacaatagatgtaggaagaacacgcgagtgtatggaatgtgatatcagg 2009
 Db 3204 ggtctatgtccagcacttctgaaagagacaggaacacactgtggaagctgatccacga 3263
 QY 2010 ggaacggt---tatctctatgtgtgtggtgatgccaaaggaaatgcccagagatgtccatcg 2066
 Db 3264 gggcggtgtccacacatctatgtgtgcgggagtctgcgaaatatggccaaagatgtgcaaaa 3323
 QY 2067 cacgttgcatacattgtcccaagaacacagggacctatggaatcatctgtgcgcaagctgc 2126
 Db 3324 cacatctcatgacattgtgctgagttcgggccccatgagcaacccaggtgtggaacta 3383
 QY 2127 agtaagaatactccaagtgtgaagaacgatatactaagagatgtctggtgatcg 2178
 Db 3384 tgttaagaagctgalgaccaaggccgctactcactcactagatgtgtggaagctag 3435

RESULT 10

AA81746

ID AA81746 standard; DNA; 3453 BP.

XX AA81746;

AC AA81746;

XX 19-OCT-1990 (first entry)

XX Plasmid pALP25.

XX Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;

XX Industrial waste; ss.

Key Location/Qualifiers

1..3453

/*tag= a

XX JP63044888-A.

XX 25-FEB-1988.

XX 12-AUG-1986; 86JP-0187713.

XX 12-AUG-1986; 86JP-0187713.

XX (AGEN) AGENCY OF IND SCI TECH.

XX WPI; 1988-094816/14.

XX P-PSDB; AAP81337.

XX Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450

XX and NADPH-cytochrome p-450 reduction enzyme

PS Disclosure: ; p; Japanese.

XX This plasmid is used in the prodn. of a chimeric fusion enzyme
 CC comprising genes for the oxidation enzyme of cytochrome p-450 and the
 CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochrome p-450
 CC reduction enzyme. See also AAN81743-85 and AAN81747-48.

XX Sequence 3453 BP; 821 A; 950 C; 947 G; 735 T; 0 other;

Query Match 7.3%; Score 192.8; DB 9; Length 3453;
 Best Local Similarity 49.08; Pred. No. 1.6e-41;
 Matches 908; Conservative 0; Mismatches 872; Indels 72; Gaps 12;

Qy	354	aattaagctcactatatttttggctactcagactggtactctgaagatttgcataaggc	413
Db	1647	aaggaaacattatctattctatgctctccagacgggaaccgctgaggatttgcacacg	1706
Qy	414	attggcagaagaatttaaggcaaggtacaagaagcagttgtttaaagttagtgcacctgga	473
Db	1707	gctgtccaagatgccaccgctacggatcggggcatgtccgcagacctgaagagta	1766
Qy	474	tgactatcagccgagatgatcaataatgaagagaaattaaagaagagttcttgggttt	533
Db	1767	tgacttgccgacctgagcagcctgctctga-----gatcgacaagtccctgggtagt	1817
Qy	534	tttcatggtagccacttatgtgtatggtagccaaactgacaaatgctgcgagattttcaaa	593
Db	1818	cttctgcatgccacatcagagagggcgaccccaagacaaatgcgagacttctatga	1877
Qy	594	atggttcaactcagaagaactgaaggaggagtggtgcttcagcaactaaacttatggttttt	653
Db	1878	ctggctg-----caggagactgacgtggacctcaactcaggtgggtcgaattgtgtatt	1928
Qy	654	tggtttggtaaccgtcaatcagcagcatttcaacaagatcgcgtagatgtggatgaaca	713
Db	1929	tggcttgggaacaagacctatgagacttcaatgccaatggcgagtgatgtggaccagcg	1988
Qy	714	actcggtaaaacaggtgcaagcgcattgttcaagtgggctcggtgacgatgatacatg	773
Db	1989	gctggagcagcttggcgccagcgcattcttgagtgggcttgggtgatgatgacgggaa	2048
Qy	774	cattgaagatgattttactgttttgcggagaattgttggactgaattggatcagttgct	833
Db	2049	cttggaaagattttcatcagtgaggaggagcagttcttgcgcagctgtgtgcagattctt	2108
Qy	834	caaaagatgagatgctgctcttcaagtgtggtacacggtatattgctactgttcttgaata	893
Db	2109	-----tgggtatgaagccactgggaggagtgctagcattcgcagtatgagctcgtgt	2162
Qy	894	cagggtagtgttccacgaactacggt---cgcggtcttggtatgataaacacataatac	950
Db	2163	ccagaagaacatggacgttagccaaggtgtacacgggtgagatgggctgtcgaagagcta	2222
Qy	951	tgtaaacggcgtatgttgcatgttatcttcacattcttcacagaccatttgttgcataca	1010
Db	2223	cgagaaccagaacaccccttcgatgtcgaagaatccattccttggtgtgtcgcacggcaa	2282
Qy	1011	aagagagctccacaacacccagctgtatagatctctgtatatacttggaggttcgacatac	1070
Db	2283	ccggaagctgaaccaagca---ctgagcggcatctaatgacactggagttggacatctc	2339
Qy	1071	aggtcttcccttccatgatgagctgagatcatgttgggttttatgtctgagaactgcga	1130
Db	2340	agactccaagatcaggtgatgaatcttggaga tcaagtggtgtgtaccacagccaatgactc	2399
Qy	1131	tgaactgtcaggaagcaggaagctgttgggtcaacccctggattgttgcgttttcaat	1190
Db	2400	agccctggtcaaccagattggggagatcctctggagctgacctggatgctcatcgtctct	2459
Qy	1191	tcacacgataaaagaagcgggttcaccccaaggaagctcatataccacctcttccocagg	1250
Db	2460	aaaca---atctcgtatggagggttcaacaag-----aagcatcgttccccctg	2504

Qy	1251	tccttgacaccttacgatactgcccctagcacgctatgctgatatcttttgaatcctctcagaaa	1310
Db	2505	cccaccacctaccgacgagccctcacctactactgacatcactaaccgcccagcac	2564
Qy	1311	ggcttctctgattgctctgtccgctcatgcatctgtaccacgtgaagcagagagattgcg	1370
Db	2565	caatgtgctctacgaactggcacagtagcagctcagagagcctcggagcaggagacctgca	2624
Qy	1371	ctttttg-----tcatacctctcgggaagaagaatgagtatccaatgggtagttgggaag	1424
Db	2625	caagatgctgctcactcctcagcgaggccaagagagctgtacctgagctgggtgggaagc	2684
Qy	1425	tcagaggagtgcttttggagatcaggcgagtttctccatcagcaaaacccctcttgggtgt	1484
Db	2685	ccggaggcacatctcctagccatcctcccaagactaaccatcactgcggccacccat---cga	2741
Qy	1485	gttcttctgctcagtagccctcgtctaccgctcctgatactattctatctcactctctcc	1544
Db	2742	ccactgtgtgagctgtgccagcctcagggccgatactactccattgctctcactctc	2801
Qy	1545	taagtttgcctcccaagaattcatgtgacgtgtgtctttagtatatggtcctcaagccctac	1604
Db	2802	caaggccaccccaactcctgcacatctgtgcgtggccgtggagtagcgaagcgaagtc	2861
Qy	1605	cggaaagggttcaccgagagtggtgttcgacatggat-----gaagcatgcagttctcca	1658
Db	2862	tggcagtgtaacaagggggtggccactagctggtcttcggccaaggaaccagcagcgca	2921
Qy	1659	ggatagctg-----ggctcctatttttgttcgaacgtcacaacttcagattccagc	1709
Db	2922	gaatggcgccgcgccttgggtaccatgttctgtgcgcaaatctcagttccgcttccctt	2981
Qy	1710	tgacctcctcaactcaattatcatggtgggacgtgtgacaggttagctcctcttcagagg	1769
Db	2982	caagtcacccacacactg tcatcattggtggcccgccactgggtatctgcccccttcatggtg	3041
Qy	1770	attcttcgcaaaaagaattggccctcaaggaataatggtgtctcaacttggcccagcagtgct	1829
Db	3042	cttcatccagaagcagcttggcttcgagagcaagcgaaggggtgggagagacgtgct	3101
Qy	1830	cttttctcggatgtgaggaatcgttaatatggaacttattatgaagcgaactaacaactt	1889
Db	3102	atactatggttgcggcgctcggatgaggaactatctgtaccgtgaagagctagccgctt	3161
Qy	1890	cgtggaaagcagaggtcatttcgagcagtagttattgctctttcacgtgaagggaagaaqaa	1949
Db	3162	ccaaagagcaggttgccttcacgcagcttaattgtggcccttttcccggggagggcccacaa	3221
Qy	1950	ggaatattgttcaacataaagatgtagagaagaacacgagatgtatggaatgtgatatcagg	2009
Db	3222	ggtctatgtccagcaccttctgaagagagacaggaacacacctgtggaagctgataccaga	3281
Qy	2010	ggacgggt---tatctctatgt	2066
Db	3282	gggctgt	3341
Qy	2067	cagttgtcattaccattgtcccaagaacacagggacccatggaatcattctgtctgcgaagctgc	2126
Db	3342	cacattctatgacattgt	3401
Qy	2127	agtaaaagaaactccaagtgtgaagacgataatctaagagatgtctgtgtgtgtgtgtgtgt	2178
Db	3402	tgtaagaagctgatgacaaaggccgctactcactcactatgtgtgtgtgtgtgtgtgtgtgtgt	3453

RESULT 11
 AAN81747
 ID AAN81747 standard; DNA; 3399 BP.
 XX
 AC AAN81747;
 XX
 DT 19-OCT-1990 (first entry)

```
XX Plasmid pALP4.
DE
XX
XX Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
KW industrial waste; ss.
XX
XX Key Location/Qualifiers
FH 1..3490
FT /*tag= a
FT
XX
XX JP63044888-A.
XX
XX 25-FEB-1988.
XX
XX 12-AUG-1986; 86JP-0187713.
XX
XX 12-AUG-1986; 86JP-0187713.
XX (AGEN ) AGENCY OF IND SCI TECH.
XX
XX WPI: 1988-094816/14.
XX P-PSDB; AAP81338.
XX
XX Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
XX and NADPH-cytochrome p-450 reduction enzyme
XX
XX Disclosure; ; Japanese.
XX
XX This plasmid is used in the prodn. of a chimeric fusion enzyme
XX comprising genes for the oxidation enzyme of cytochrome p-450 and the
XX nicotinamide adenine dinucleotide phosphate (NADPH)-cytochrome p-450
XX reduction enzyme. See also AAN81743-86and AAN81748.
XX
XX Sequence 3399 BP; 818 A; 941 C; 931 G; 709 T; 0 other:
XX
Query Match 7.2%; Score 191.4; DB 9; Length 3399;
Best Local Similarity 49.6%; Pred. No. 3.8e-41;
Matches 836; Conservative 0; Mismatches 786; Indels 63; Gaps 11;
QY 521 agctcttggtgttttctatggttagcacttatgtgtatggtgagcacaactgacaaatgctg 580
DB 1751 agtccctggtagtcttctgcatggtccacatacggagagggcgaccccccagggacaatggcg 1810
QY 581 cgaattttacaaatggttcactcaggaacatgaagaggagaggtgttcagcaactaa 640
DB 1811 aggaacttctatgactggct-----gcaggagactgactggacacctactggtgggtca 1861
QY 641 ctatggtgttttgggttggttaaccgtcaatacagacgacatttcaacaagatcgcggtag 700
DB 1862 agttgctgtattgtgttgggaacagacactatgacacactcaatgccatgggcaagt 1921
QY 701 atgtggtgagcaactcgtgtaacaaagtgcaaaagcgcaattgttcaagtggggctcggtg 760
DB 1922 atgtggaccagcgctggagcagctggcgccagcgcatctttagttggcccttggtg 1981
QY 761 acgatgataactgattgaagatgatttactgttggcgagaaattgttgtgagactgaat 820
DB 1982 atgatgacgggaacttgaagaggatttctatcactggtgagggagcagttcttggcagctg 2041
QY 821 tggatcagttgtcacaagatgagatgctgctccctcactggtcactacacgtattgtcta 880
DB 2042 tgtgaggttctt-----tggggttagaagccacttggggaggtcgagacttccccagt 2095
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DB 2096 atgagctgctgtgtccacgaagacatggacgttagccaaggtgtacacgggtgagatgggcc 2155
QY 938 aacacataaatactgctaacggcgatgttgtgaatttgatatcttccatctcttcgaacaaca 997
DB 2156 gtctgaagagctacgagaaacgaacccccctctgatgtgtaagaatccatcttctggctg 2215
QY 998 ttgttgcatacaaaagagctcccaacaaacccaaagctgtgatgacctgtatcacatctgg 1057
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Db 2216 ctgtacccgccaacccggaagctgaaaccaaggca---ctgagcgcgcatctcaatgcacctgg 2272
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QY 1646 atgcagttcctcagatagctg-----ggtcctctattttgttcgaacgtcaaac 1696
Db 2855 aaccggcggcgagaaatggcgccgcgcctgtgtaccctatgtctgtgcgaactctcagt 2914
QY 1697 tcaagtaccagctgacccctcaactccaatatcatggtgggaccctggtacaggttag 1756
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QY 1757 ctcttccagaggaattctgcaggaaagaatggccctcgaaggaataatggtctcaacttg 1816
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Db 3035 gagagacgtgctaactatggtccgctcgctcgatgagagactatctgtaccctggaag 3094
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QY 1937 aaggggaagaagaatatgttcaacataaagatgatggagaagaacacgagtgatgga 1996
Db 3155 agcaggcccaagaagttctatgtccagacacttctgaagagagacagggaaacacctgtgga 3214
QY 1997 atgtgatatcaggggacaggt---tatctctatgtgtgtgtgatgccaaagggaatggcca 2053
Db 3215 agctgatccagcagggcggtgccccacatctatgtgtgogggatgctcgaaatatggcca 3274
QY 2054 gagatgctcatcgacgttgcataccattgtcccaagaacaggaccatgggaatcatctg 2113
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Db 3275 aagatgtgtcaaaacacattctatgacattgtgtggtgagttcggtggccatgagacacccc 3334
 Qy 2114 ctgcccagctgcagtaagaacacccaagttgaagaacgatatcaatgaagatgtctgtgt 2173
 Db 3335 aggcgtgtgactatgttaagaagctgtagaccaagggccgctactactactagatgtgtga 3394
 Qy 2174 gatcg 2178
 Db 3395 gctag 3399

RESULT 12
 AAN70925
 ID AAN70925 standard; DNA; 2037 BP.
 XX
 AC AAN70925;
 XX
 DT 07-MAY-1991 (first entry)
 XX
 DE
 XX
 XX Sequence encoding NADPH cytochrome P-450 reductase.
 XX
 XX Yeast; Fpt; analgesic; antipyretic; ds.
 XX
 XX JP62104582-A.
 XX
 PD 15-MAY-1987.
 XX
 XX 31-OCT-1985; 85JP-0242772.
 XX
 PR 31-OCT-1985; 85JP-0242772.
 XX
 XX (AGEN) AGENCY OF IND SCI TECH.
 XX
 XX WPI: 1987-173699/25.
 DR P-PSDB: AAP70578.
 XX
 XX Plasmid p-ARM1 simultaneously expressing rat hepato-cytochrome
 PT P-450MC - and NADPH-cytochrome P-450 reductase in yeast and yeast
 PT contg. p-RAM 1
 XX
 PS Disclosure; Fig 4; 9pp; Japanese.
 XX
 CC The sequence may be used to construct a plasmid which may
 CC transform a yeast expression system to produce both rat hepato-
 CC cytochrome P-450MC and NADPH cytochrome P-450 reductase (Fpt). This
 CC is useful in removal of organic compounds from toxic waste water.
 CC The yeast is capable of hydroxidising the p-position of
 CC acetanilide useful in the production of acetaminophenes which are
 CC antipyretics and analgesics.
 XX
 SQ Sequence 2037 BP; 481 A; 568 C; 588 G; 400 T; 0 other;

Query Match 7.2%; Score 191.2; DB 8; Length 2037;
 Best Local Similarity 49.0%; Pred. No. 3.3e-41;
 Matches 907; Conservative 0; Mismatches 873; Indels 72; Gaps 12;

Qy 354 aattaagctcactatattttttgtactcagactgtgtactgaagatttgcataagc 413
 Db 231 aaggacattatcgatctctatggtctccacagcgggaaccgctgaggatttgcacacg 290
 Qy 414 attggcagaagaataaggcacaagtacaaagacagttgttaagtagttgacctgga 473
 Db 291 gctgtccaaagatgccaccgctacggatgctggggcagtgccgcagaccctgaagagta 350
 Qy 474 tgcattatgcagccgaggatgatcaataatgaagagaaaataaagaagagtttgggtgtt 533
 Db 351 tgacttggccgacctgagcagcctgctga-----gacgcacaagtcctggtagt 401
 Qy 534 ttctatgttagccacttatgttgatggtgagcccaactgacaaatgctgcgagattttacaa 593
 Db 402 ctcttgcattgcccacatcagagagggcgaccccccagacaaatgcgaggacttctatga 461

Qy 594 atggttctactcaggaaacatgaaaggggagtggtcttcagcaactaaacttattggtgtttt 653
 Db 462 ctggctg-----caggagactgacgtggaacctactcactgggtcgaagtttgcgtattt 512
 Qy 654 tgggttgggttaacctcaatcagcagcatttcaacaagatcgcggtagatgtgtgagagca 713
 Db 513 tgggtctgggaacaagacctatgacacttcaatgccatggcgaagtatgtggaaccagcg 572
 Qy 714 actcggtaacaaggtgcaaaagcgcattgttcaagtggggctcgcgtgacgagatgacaaatg 773
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 Qy 774 cattgaagatgatttttaactgcttggcggagaaattgtgtgagcgaattgggacagttgct 833
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 Qy 834 caaagatgagagatgctgctcttcagtggtctacacgcgtatattgctactgttctcgaata 893
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 Qy 951 tgcataacggcgtgtgttcatttgatattctcctcctctgcagaaacattgttgcataaca 1010
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 Qy 1251 tcttgaccttaagatctgcctcagcgcgtatctgctgatttggaaacctccctagaaa 1310
 Db 1089 cccaaccctaccgcacggccctcactactactactcactgacatacactaaccgccagcgc 1148
 Qy 1311 ggcctctctgattgctgtcgcgtcactgcatctgtaccagtgaaagcagagagattggcg 1370
 Db 1149 caatgtgcttacgaactggcacagtagcctcagagcctcgagcagcagagcactgca 1208
 Qy 1371 ctttttg-----tcatacctcttgggaagaatgagtagttcaaaaatgggtgagtggaag 1424
 Db 1209 caagatggtcgtcatcctcagggcagggcaagagagctgtacctgagctgggtggtggaagc 1268
 Qy 1425 tcagaggagcttttggagatcatggtccgagtttccatcagcaaaacccctcttctgtgt 1484
 Db 1259 cggaggagcacatctcagcatctcctcaagactaccatcactgctggggccaccat---cga 1325
 Qy 1485 gtcttttgcgcagtagccctcgtctaccgctcgcatactattctatctatctctctcc 1544
 Db 1326 ccacctgtgtgagctgtgcacgcctcagggccgcgatactactcctatctgctatctctc 1385
 Qy 1545 taagtgttgcctcccaagaattcatgtgacgtgtgcttttagtatatggttcaaaagccctac 1604
 Db 1386 caaggtccaccacccactcctgtcacatctgtgccgtggcgtggagtagcgaagcgaagtc 1445
 Qy 1605 cggaaaggttccaccgagagtggtgtccacatggat-----gaagcatgcagttctccca 1658
 Db 1446 tggccgagtgaaacaaggggtggccactagctggtctcgggcgaaggaaccagcggcgga 1505
 Qy 1659 ggatagctg-----ggctccctattttgttcgaacgtcaaaacttccaaagtaccagc 1709

Db 1506 gaatggcgccgcccgtgtaccatgttcgtgcgaaatcagttccgcttgcctt 1565
 Qy 1710 tgaccctcaactcaattatcatgttggaacctggtacagaggttagctccttcagagg 1769
 Db 1566 caagtccaccacacctgtcatgtgtggcccgccactggattgccctttcatggg 1625
 Qy 1770 attctgcaggaagaatggccctcaaggaaatggtgtctcaactggccagcagtgct 1829
 Db 1626 ctctatcaggaaacagcttggtctcgagagcaagcaggaggtggagagacgtctgt 1685
 Qy 1830 ctttttcggataggaatcgttaatgatggaacttattatgaagacgaactaaacaatt 1889
 Db 1686 atactatgctcgcgctcggtgaggaactatctgtaccgtgaagactagccgctt 1745
 Qy 1890 cgtgaaacagagagcatttcggagactagttattcccttttcaactggaagggaagaa 1949
 Db 1746 ccacaagacggtgcctcaacgacgttaattgtcccttttcccgggagcggccacaa 1805
 Qy 1950 ggaatatgtcaacataaagatgatggagaaacacgagatgatgaatgtgatatacagg 2009
 Db 1806 ggtctatgtccagacccttgaagagagacagggaacacacctgtggaagctgatccaga 1865
 Qy 2010 ggacggt---tatctctatgtgtgtgtgacgtcccaagggaatggccagagatgtccatcg 2066
 Db 1866 gggcggtgccacatctatgtgcgggatgtctgaaatatgccaagatgtgcaaaa 1925
 Qy 2067 cacgttgataccattgcccaagaacagaggaccatgaatcatctgtgcgcaagctgc 2126
 Db 1926 cacattctatgacattgt 1985
 Qy 2127 agtaagaacatcccaagttgaagacgatatctaaagagatgtctgtgtgtgtgtgtgtgt 2178
 Db 1986 tgttaagaagctgatgaccaaggcgctactcaactagatgtgtggagctag 2037

RESULT 13
 AAN81744
 ID AAN81744 standard; DNA; 3453 BP.
 XX
 AC AAN81744;
 XX
 DT 19-OCT-1990 (first entry)
 XX
 DE Plasmid pALP1.
 XX
 KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
 KW industrial waste; ss.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3453
 FT /*tag= a
 XX
 PN JP63044888-A.
 XX
 PD 25-FEB-1988.
 XX
 PF 12-AUG-1986; 86JP-0187713.
 XX
 PR 12-AUG-1986; 86JP-0187713.
 XX
 PA (AGEN) AGENCY OF IND SCI TECH.
 XX
 DR WPI; 1988-094816/14.
 DR P-PSDB; AAP81335.
 XX
 PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
 PT and NADPH-cytochrome p-450 reduction enzyme
 XX
 PS Disclosure; ; P; Japanese.
 XX
 CC This plasmid is used in the prodn. of a chimeric fusion enzyme
 CC comprising the genes for the oxidation enzyme of cytochm. p-450 and the

CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochm. p-450
 CC reduction enzyme. See also AAN81743 and AAN81745-48.
 XX
 SQ Sequence 3453 BP; 817 A; 950 C; 946 G; 740 T; 0 other;
 Query Match 7.2%; Score 191.2; DB 9; Length 3453;
 Best Local Similarity 49.0%; Pred. No. 4.3e-41;
 Matches 907; Conservative 0; Mismatches 873; Indels 72; Gaps 12;
 Qy 354 aattaagtcactatatttttggactcagactggtactgctgaagatttggtaagcg 413
 Db 1647 aaggaaacattatcgtattctatgctccagagcggaacccgctgaggaattggccaacg 1706
 Qy 414 attgcagaaagaattaaaggcaaatgataaagaacgagtgtttaaagttagtgaactgga 473
 Db 1707 gctgtcccaaggatgccaccgctacgggtatcggggcatgtccgcagaccctgaagagta 1766
 Qy 474 tgactatgcagccgaggtatgataatgaagagaaaattaaagaagaagatcttttgggttt 533
 Db 1767 tgactggccgacctgagcagcctgcctga-----gatcgacaagtcctcctgtagt 1817
 Qy 534 ttctatgttagccacttatgtgtgtagccaaactgacaatgctgogagattttacaa 593
 Db 1818 cttctgcatggccacatacgagagggggaaccccggaacaatgcgcaggaactctatga 1877
 Qy 594 atggttcaactcaggaaacatgaaggagggagagtggttcagcaactaatatttggtttt 653
 Db 1878 ctggctg-----caggagactgaactggagcctcactcactcactcactcactcactcact 1928
 Qy 654 tggtttggtaaccgtcaatcagcagcatttcaacaagatcgcggtagatgtgtgtagagca 713
 Db 1929 tggctctgggaacaagacctatgacacttcaatgccatgggcaagtatgtgagaccagcg 1988
 Qy 714 actcgttaacaaggtgcaaaagcagcttgttcaagtggggctcgtgtagcagatgataatg 773
 Db 1989 gctggagcagctggcgccacgcagctctttagttggccttgggtgatgtagcgggaa 2048
 Qy 774 caatgaagatgattttactgcttggcgagaattgtgtgagctgaattggatcagttgct 833
 Db 2049 ctggaagaggatttcaatcagctggaggagcagttctcctggcagctgtgtgcgagttct 2108
 Qy 834 caaagatgaggatgctgctcctcagtggtacacgcgtatatattgctactgttccctgaata 893
 Db 2109 -----tggggtagaagccactgggagggagtcgagcattccgagtagtgcgtggt 2162
 Qy 894 cagggtagtgattcacgaaactacggt---cgcggtcgtggtatgataaacaacataaatac 950
 Db 2163 ccacgaagacatggagctagccaaggtgtacacgggtgagatggcgctctgaagagcta 2222
 Qy 951 tgctaacggcgatgtgcatgttgatattctccactctgcagaaacattgtgtgctcaaca 1010
 Db 2223 cgagaaccagaaacccctctcgatgctaagaatccattcctcgtgctgtccacgcca 2282
 Qy 1011 aagagagctccacaaccccaagctctgatagatccctgtatacatctggagctcgacatctc 1070
 Db 2283 ccggaagctgaaccaaggca---ctgagcggcatctaatacgaccctggaggttggaatctc 2339
 Qy 1071 aggtctcttcccttacaatgagactggagatcatgttgggttttatgtctgagaactcgga 1130
 Db 2340 agactccaagatcaggtagaattctggagatcacgtggctgtgtaccacgccaatgactc 2399
 Qy 1131 tgaactgtcgagggaagcagggaagcgtgtgggtcaacccctggagtttgcgttttcaat 1190
 Db 2400 agcctgtgtcaaccagattggggagatcctggagctgacctggatgcatcatgtctct 2459
 Qy 1191 tcacgcgataaagaagcgggtcccccaggggaagctcattaccacctccttcccagg 1250
 Db 2460 aaaaa---atctcgatgaggagtcacaaag-----aagcatccgttcccctg 2504
 Qy 1251 tcttgcaccttaacatctgccttagcagcgtatgctgatcttttgaatcctcctagaaa 1310
 Db 2505 ccccccacctaccgcacggccctcacctactactgacatcactggaacataaccgcccagcac 2564

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Oy 1311 ggcttctctgattgctctgctcgtcatctgtacccagtgaaagcagagagattgcg 1370
    || || || || || || || || || || || || || || || || || || || ||
Db 2565 caatgtctctacgaactggcagcagtagcctcagagccctcgagcagagcactgcga 2624
    || || || || || || || || || || || || || || || || || || || ||
Oy 1371 ctttttg-----tcatacctctgggaaagaatagattatcaaatgggtagttgggaag 1424
    || || || || || || || || || || || || || || || || || || || ||
Db 2625 caagatggcgtcatctcctcagcgagggcgaaggagctgacctgagctgggtggtggaagc 2684
    || || || || || || || || || || || || || || || || || || || ||
Oy 1425 tcaagagagctcttttggagatcagcgagtttccatcagcaaaacccctcttgggtg 1484
    || || || || || || || || || || || || || || || || || || || ||
Db 2685 ccggagggcacatctagccatctcccaagactaccaccaactcgcgccaccocat---cga 2741
    || || || || || || || || || || || || || || || || || || || ||
Oy 1485 gttctttgctcagtagccctcgcttaccgctcgtactactattctatctatctctccc 1544
    || || || || || || || || || || || || || || || || || || || ||
Db 2742 ccactgtgtgagctgtgcacgctcagcgccgatactactcattgctcctactcctc 2801
    || || || || || || || || || || || || || || || || || || || ||
Oy 1545 taagtgttctcctcaagaattcatgtgacgtgtgctttagtatatgtgtcaaaagccctac 1604
    || || || || || || || || || || || || || || || || || || || ||
Db 2802 caaggtccaccaccaactcctgtgacatctgtgccgtggcgtggagtagcgaagcgaagtc 2861
    || || || || || || || || || || || || || || || || || || || ||
Oy 1605 cggaaaggttaccgagagagtggttcacatggat-----gaagcatgagttcctca 1658
    || || || || || || || || || || || || || || || || || || || ||
Db 2862 tggccagtgaaacaagggggtggccactagctggcttcggccaaaggaaacccagcaggcga 2921
    || || || || || || || || || || || || || || || || || || || ||
Oy 1659 ggatagctg-----ggctcctattttgttcgaacgtcaaaacttcaagtaccacgc 1709
    || || || || || || || || || || || || || || || || || || || ||
Db 2922 gaatggcgcgccctggtaaccatgttcgtgcgaatactcagttccgttgcctt 2981
    || || || || || || || || || || || || || || || || || || || ||
Oy 1710 tgacctccaactccaattatcatgtgtggacctgttacaggggttagctctcttcagagg 1769
    || || || || || || || || || || || || || || || || || || || ||
Db 2982 caagtcaccaccacctgtcatcatgtgtggcccgccgactgggtgggagacgtctgt 3041
    || || || || || || || || || || || || || || || || || || || ||
Oy 1770 atttctcaggaagaatggccctcaagaaatggtgctcaacttggcccgagcagtgct 1829
    || || || || || || || || || || || || || || || || || || || ||
Db 3042 ctctcatcaggaaacagagcttggtctcgagagcaaggcgaagggtgggagacgtctgt 3101
    || || || || || || || || || || || || || || || || || || || ||
Oy 1830 ctttttcgagtaggaatcgtaatatgacttcttattatgaagacgaactaaacaactt 1889
    || || || || || || || || || || || || || || || || || || || ||
Db 3102 atactatggtcgccgctcggtgagactatctgtaccgtgaagagtagccgctt 3161
    || || || || || || || || || || || || || || || || || || || ||
Oy 1890 cgtggaacagagagtcatttcgagctagttattgccttttcacgtgaaggggaaagaa 1949
    || || || || || || || || || || || || || || || || || || || ||
Db 3162 ccacaagacggtgccctcagcagctaatgtgcttcttccggggagcagggcccaaa 3221
    || || || || || || || || || || || || || || || || || || || ||
Oy 1950 ggaatatgtcaacataagatgatggagaaacacgagtgatggaatgtgatcaggg 2009
    || || || || || || || || || || || || || || || || || || || ||
Db 3222 ggtctatgtccagacacctctcgaagagagacagggaacacctgtgtggaagctgatccaga 3281
    || || || || || || || || || || || || || || || || || || || ||
Oy 2010 ggaacggt---tatctctatgtgtgtgtgtagtcccaagggaatggccagagatgtccatcg 2066
    || || || || || || || || || || || || || || || || || || || ||
Db 3282 gggcggtgccacatctatgtgtcggggagtgctcgaataatggccaaagatgtgcaaaa 3341
    || || || || || || || || || || || || || || || || || || || ||
Oy 2067 cactgtgtatacatttgcccaagaacagggaccctatgaatactctgtgcggaagctgc 2126
    || || || || || || || || || || || || || || || || || || || ||
Db 3342 cacattctatgacattgtgctgagttcgggccccttgagcagacccactgtgtgacta 3401
    || || || || || || || || || || || || || || || || || || || ||
Oy 2127 agtaagaacatcccaagttggaagacgatatctaagagatgtctggtgatcg 2178
    || || || || || || || || || || || || || || || || || || || ||
Db 3402 tgttaagaagctgatgaccaaggccgctactcactcactagatgtgtggaagctag 3453
    || || || || || || || || || || || || || || || || || || || ||
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RESULT 14

AA70605

ID AA70605 standard; cDNA; 2450 BP.

XX AC

XX AA70605;

XX AC

DT 26-APR-1991 (first entry)

XX AC

DE Plasmid pRF1 encoding rat liver NADPH cytochrome P450 reductase.

XX AC

KW P-450MC; Fpt; Saccharomyces cerevisiae AH22; ds.

```
XX Rattus sp.
XX OS
XX FH Key Location/Qualifiers
XX FT CDS 41..2077
XX FT /*tag= a
XX PN JP62019085-A.
XX PD 27-JAN-1987.
XX PF 05-JUL-1985; 85JP-0146653.
XX PR 05-JUL-1985; 85JP-0146653.
XX PA (AGEN ) AGENCY OF IND SCI TECH.
XX XX
XX DR WPI; 1987-062501/09.
XX DR P-PSDB; AAP70380.
XX PT New plasmid typically pRF1 - has total coding region of rat liver
XX PT NADPH cytochrome p-450 reductase gene
XX XX
XX PS Disclosure; Fig 4; 14pp; Japanese.
XX CC The rat liver NADPH-cytochrome P-450 reductase gene may be used to
XX CC transform a yeast expression system (S.cerevisiae AH22) for the
XX CC production of rat liver Fpt and P-450MC of high oxidation activity.
XX SQ Sequence 2450 BP; 572 A; 689 C; 493 T; 0 other;

Query Match 7.1%; Score 187.6; DB 8; Length 2450;
Best Local Similarity 48.7%; Pred. No. 3.4e-40;
Matches 913; Conservative 0; Mismatches 889; Indels 72; Gaps 12;

Oy 354 aattaagctcactatatttttggctactcagactgtgactgtgtaaggatttggtaagc 413
    || || || || || || || || || || || || || || || || || || || ||
Db 271 aaggaaactattcgtattctatgctcccgagcggaacgcgtgagggatttggccaacg 330
    || || || || || || || || || || || || || || || || || || || ||
Oy 414 atggcagaagaatttaaggcaagtaagaagcagttgtttaagtagtgtaacctgga 473
    || || || || || || || || || || || || || || || || || || || ||
Db 331 gctgtccaaaggatgccaccgctacgggagtgagggtgctgcgcgagccctgaagagta 390
    || || || || || || || || || || || || || || || || || || || ||
Oy 474 tgactatgcagccgagagtgatcaatataagagaaattaaagaagagtccttgggtgtt 533
    || || || || || || || || || || || || || || || || || || || ||
Db 391 tgacttggccgacctgagcagcagctgctga-----gatcgacaagtccttgtagt 441
    || || || || || || || || || || || || || || || || || || || ||
Oy 534 ttctatggtagccacttatgtggtggtgagccaaactgacaatgctgcgagattttacaa 593
    || || || || || || || || || || || || || || || || || || || ||
Db 442 ctctctgcatggccacatacgagagggcgaccccgagcaatgcgaggaacttctatga 501
    || || || || || || || || || || || || || || || || || || || ||
Oy 594 atgggtcactcaggaacatgaaggggagagtggttcagcaactaacattatggtgtttt 653
    || || || || || || || || || || || || || || || || || || || ||
Db 502 cgggtgtg-----caggagactgacgtgacctcactgggttcaagtttgcgtatt 552
    || || || || || || || || || || || || || || || || || || || ||
Oy 654 tggtttggtaaacgctcaatcacagcatctcaacaagatcgcggtagatgtggatgagca 713
    || || || || || || || || || || || || || || || || || || || ||
Db 553 tggcttgggaacaagacctatgacactcaatgcatgctgggcaagatgtggaccagag 612
    || || || || || || || || || || || || || || || || || || || ||
Oy 714 actcggtaacaaggtgcaaacgcgaatttccaagtggggctcgggtgacgatgataatg 773
    || || || || || || || || || || || || || || || || || || || ||
Db 613 gctggagcagcttggcgccagccgatcttctgagtggtggccttgggtgagtgacgggaa 672
    || || || || || || || || || || || || || || || || || || || ||
Oy 774 cattgaagatgattttactgcttggcgagaattgttggactgaattggatcagattgct 833
    || || || || || || || || || || || || || || || || || || || ||
Db 673 cttggaagaggatttctcactcactggtggaggagcagttctgtgagagcttctt 732
    || || || || || || || || || || || || || || || || || || || ||
Oy 834 caaagatgaggtgcttctcctcactggtgctacacccgtatattgctactgcttcttgaata 893
    || || || || || || || || || || || || || || || || || || || ||
Db 733 -----tggggtagaagccactggggagagtgagcagcattcgcgaatgatgagctgtggt 786
    || || || || || || || || || || || || || || || || || || || ||
Oy 894 cagggttagtgattcacgaaactacggt---cgcggctctgtgatgataaacacataaac 950
    || || || || || || || || || || || || || || || || || || || ||
```

Db 787 ccacgaagacatggcgtagcagcaaggtgtacacgggtgagatgcgcgctcgaagacta 846
 Qy 951 tgcctaagcgcgtatgttgattgatattctcatctctgcagaaacattgtgtgctcaaca 1010
 Db 847 cgagacagagaaccccccttcgtactgaagatccattccttggtgctgtccaccgcaa 906
 Qy 1011 aagagagctcccaaaccaagctgatagatccctgtatcacatctcggagttcgacatctc 1070
 Db 907 cgggaagctgaaccagaagca---ctgagcggcatctaataatgcacctggagttggacatctc 963
 Qy 1071 aggcctctcccttaacatatgagactggagatcatgtgtggtgtttatgtcgagaactggga 1130
 Db 964 agactccaagatcaggtatgaatcgtgagatcaacgtggtgtgtaccacgaaccaatgactc 1023
 Qy 1131 tgaactgtcaggaagcaggaagactgtgttggtgtcaacccctggattgtgttttcaaat 1190
 Db 1024 agccctggtcaaccagattgggagatcctggtgagctgacctggatgtcatcatgtctct 1083
 Qy 1191 tcacagcataaaagacgggtcaccacaggaagctcattaccacotctttccacgg 1250
 Db 1084 aaaca---atctcgatgggagtcacaaga-----aagcatccgttcccctg 1128
 Qy 1251 tccctgcaccttaecgatctgcctcagcagctatgctgatcttttgaatccctccctagaaa 1310
 Db 1129 cccaaccactaccgcagcgcctcactactactacactgacatcaactaaccgcacgcac 1188
 Qy 1311 ggcctctctgattgtctgtccgcctcagctatctgtacatcttgaatccctccctcattgcg 1370
 Db 1189 caatgtctctacgaactggcagactagcctcagcagcctcgagcaggaagcactgca 1248
 Qy 1371 ctttttgcatacctct-----gggaagaatgagtattcaaaatgggtagttgggaag 1424
 Db 1249 caagatggcgtcatcctcagcggagggcaagagagctgtacctgagctgggtggtggaagc 1308
 Qy 1425 tcagagagagcttttggagatcagcgcaggtttccatcagcaaaacccctcttgggtgt 1484
 Db 1309 cggaggaacatctcctagcactcctcagagactaccatacctcagcggccacccat---cga 1365
 Qy 1485 gtctttgctgcagtagccctcgtcttaaccgctcgtactactatctctcctctctcc 1544
 Db 1366 ccacctgtgtgagctgtgcacgcctgcagcgcgcgatactactcctcctgctcctcctc 1425
 Qy 1545 taagtttgcctcccaagaattcatgtgacgtgtgcttttagtatatgttcaaaagccctac 1604
 Db 1426 caaggtccaccccaactccgtgcacatctgtccgtgcccgtggagtacgaagcgaagtc 1485
 Qy 1605 cggaaaggttccaccgagaggtgtgtcgacatggat-----gaagcatgcagttctccta 1658
 Db 1486 tggcccaatgaacaagggtgtggccactagctggttcggcccaagggaaccagcagggcga 1545
 Qy 1659 ggaatagctg-----ggctctatttttgttcgaacgtcaaaacttcaagttaccacgc 1709
 Db 1546 gaatggcggcgcgcgcctcgtgtaccatgttgctgcgaaaatctcagttccgcttgcttt 1605
 Qy 1710 tgacctccaaactcaattatcatgtgtggaccttggtacaggggttagctcctttcagagg 1769
 Db 1606 caagtccaccacacgtctcatatgtgtggcccgccgactggtggtccctttcctatggg 1665
 Qy 1770 atttctcaggaagaatggccctcaaggaatggtgtcctcaacttggcccgagcagtgct 1829
 Db 1666 ctctaccaggaacagacttggcttcgagagcaagcagagaggtgggagagacgtcgt 1725
 Qy 1830 ctttttcggatgtagaatactgtaatatggaacttctattatgaagcagcaactaaacaatt 1889
 Db 1726 atactatggtcgcgcgcctcggatgagagactatctgacogtgaagagctagcccgctt 1785
 Qy 1890 cgtgaaacaggaagactatccgagactagttattgccttttcaactgaaggggaaagaaa 1949
 Db 1786 ccacaaggaagcgtgcccctcaacgcagcttaatgtggccttttcccgggagcagggcccaaa 1845
 Qy 1950 ggaatatgtcaacataagatgatgagaaagcaacgcgatgtgatggaatgtgatcagg 2009

Db 1846 ggcttatgtccagcaccttctgaagagagacagggaacacctgtggaagctgatccacga 1905
 Qy 2010 ggaacgt---tatctctatgtgtgtgtgatgccaaaggaatggccagagatgtccatcg 2066
 Db 1906 gggcgggtgccacatctatgtgtgcggggtgctcgaaaatggccaaagatgtgcaaaa 1965
 Qy 2067 cagctgtgataccattgcccagaacagagggacccatggaatcatctgtgcccgaagctgc 2126
 Db 1966 cacattctatgacattgtgtgctgagttcggcccatgaggacacacccagctgtggaacta 2025
 Qy 2127 agtaagaacatcccaagtttgaagaacgatatctaaagagatgtctgtgatcgaatgtgc 2186
 Db 2026 tgttaagaagctgatgaccaagggccgctactcactagatgtgtgagctagtagctacc 2085
 Qy 2187 ttgcgaagtccctc 2200
 Db 2086 agcctcccaacctc 2099
 RESULT 15
 AAN81745
 ID AAN81745 standard; DNA; 3489 BP.
 XX AC AAN81745;
 XX DT 19-OCT-1990 (first entry)
 XX DE Plasmid pALP17.
 XX KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
 KW industrial waste; ss.
 XX FH Key Location/Qualifiers
 FT CDS 1..3490
 FT /*tag= a
 XX PN JP63044888-A.
 XX PD 25-FEB-1988.
 XX PF 12-AUG-1986; 86JP-0187713.
 PR 12-AUG-1986; 86JP-0187713.
 XX PA (AGEN) AGENCY OF IND SCI TECH.
 DR WPI; 1988-094816/14.
 DR P-PSDB; AAP81336.
 PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
 PT and NADPH-cytochrome p-450 reduction enzyme
 XX Disclosure; ; p; Japanese.
 PS This plasmid is used in the prodn. Of a chimeric fusion enzyme
 CC comprising genes for the oxidation enzyme of cytochrome p-450 and the
 CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochrome p-450
 CC reduction enzyme. See also AAN81743-84 and AAN81746-48.
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Job time: 6458 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:28:30 ; Search time 2203.48 Seconds
(without alignments)
12918.460 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	371.4	14.0	658	10	AW256561 EST304698
5	366.6	13.8	683	10	AW398515 EST309015
6	357.6	13.5	824	11	BG319913 Zm03_08d1
7	350.6	13.2	559	11	BG362645 sac06g11
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ALIGNMENTS

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DEFINITION	AI730999
ACCESSION	AI730999.1 GI:5049851
VERSION	EST.
KEYWORDS	upland cotton.
SOURCE	Gossypium hirsutum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE	1 (bases 1 to 659)
AUTHORS	Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
TITLE	ESTs from developing cotton fiber
JOURNAL	Unpublished (1999)
COMMENT	Contact: Ben Burr Biology Department Brookhaven National Laboratory Upton, NY 11973, USA Tel: 516-344-3396 Fax: 516-344-3407 Email: burr@bnl.bnl.gov Seq primer: T3 Primer. Location/Qualifiers 1. .659 /organism="Gossypium hirsutum" /cultivar="Acala Maxxa" /db_xref="taxon:3635" /clone_lib="Six-day Cotton fiber" /tissue_type="Immature fiber" /dev_stage="Six days post anthesis" /lab_host="XL1-Blue"
FEATURES	source

with Sinorhizobium meliloti		Unpublished (1999)		Contact: VandenBosch K		Department of Biology		Texas A&M University		College Station, TX 77843-3258, USA		Tel: 409 845 7707		Fax: 409 845 2891		Email: kate@mail.bio.tamu.edu		Texas A&M University name: T267798e TIGR sequence name: MTIAZ18TK		More information is available at: http://chrysie.tamu.edu/medicago		Seq primer: SKmod (CTA gaa cta gta gat cc).																																																																																																																									
JOURNAL		COMMENT		BASE COUNT		ORIGIN		Query Match		Best Local Similarity		Matches 536; Conservative		14.9%; Score 394; DB 11; Length 775;		71.8%; Pred. No. 2e-86;		Mismatches 195; Indels 15; Gaps 1;		198 a 163 c 181 g 233 t		BASE COUNT		ORIGIN																																																																																																																							
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JOURNAL COMMENT		with Sinorhizobium meliloti	
		Unpublished (1999)	
		Contact: VandenBosch K	
		Department of Biology	
		Texas A&M University	
		College Station, TX 77843-3258, USA	
		Tel: 409 845 7707	
		Fax: 409 845 2891	
		Email: kate@mail.bio.tamu.edu	
		Texas A&M University name: T267798e TIGR sequence name: MTIAZ18TK	
		More information is available at: http://chrystie.tamu.edu/medicago	
		Seq primer: Samod (CTA gAA CTA gtg gAT CC).	
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cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in SOLR cells."

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ORIGIN

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ORGANISM Lycopersicon pennellii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 683)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E.,
Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii
,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin
,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
trichomes
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Source
1..683
/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT2K2"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
BASE COUNT      168 a 160 c 160 g 195 t
ORIGIN

Query Match      13.8%; Score 366.6; DB 10; Length 683;
Best Local Similarity 72.0%; Pred. No. 1.1e-79;
Matches 493; Conservative 0; Mismatches 189; Indels 3; Gaps 1;

QY 887 ctgaatacagggtagtgattcacgaaactacggtcgcgctcgtggtgataaacacataa 946
Db 2 CTGAATATCGTTGGTTATCCATGATACCACCTAT---GAGTCTTGAGGATAGCATGCAG 58

QY 947 atactgctaacggcgatgttgcatgttgatatctccatcctcgtcagaacattgtgctc 1006
Db 59 GCATGGCTTAATGGTAATACACATATGATCCACCACCATGTCACACCCCATGCAAAAGTCAATGTGGCTG 118

QY 1007 acaaaagagagctccacaaacccaaagctcgtatagatcctgtatatacatctggagttcgaca 1066
Db 119 TTCAGAGAGAGCTTCACACACCCGAGCTGTGCTCATGCATACACTTGGAGTTTGATA 178

QY 1067 tatcaggctcttcccttcacatatgagactggagatcatgttggtgtttatgctgagaact 1126
Db 179 TATCTGGCACTGGGATTTCTTATGAAACAGGAGATCATCTGGGTGTTTATGCTGAAAAATT 238

QY 1127 gcgatgaaactcaggaagacagggaagctgttgggtcaacccctcgtattcgtgtttt 1186
Db 239 CTGAAGATACTGTTGAGGAAGCTGCGAGATTGCTGGGGCAGTCATTTAGACTTTGATATTCT 298

QY 1187 caattcacacggataaagaagacgggtgcaccccggaagcctcattaccacctcttccc 1246
Db 299 CTATTTCATACCACAAAGGAGGATGTTACAGCTGGAGAGGCTCGCTACCCCACTTTTC 358

QY 1247 caggctccttgacccttaogatcgtccctagcagcgtatgctgatcttttgaatcctccta 1306
Db 359 CTGGCCCTGCACCTCTACGTCGTGCACCTTGCCTGTTTATGAGATCTTCTGAATCCACCGC 418
```


Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE JOURNAL COMMENT

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com

High quality sequence stop: 487.

FEATURES

source

1. .559
Location/Qualifiers
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl040-3790"
/clone_lib="Gm-cl040"
/tissue_type="Hypocotyl and Plumule, germinating seeds"
/lab_host="DH10B"
/note="Vector: pT73Pac (Pharmacia); Site_1: EcoRI; Site_2: NotI; This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestions with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT73-pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 123 a 135 c 129 g 172 t

ORIGIN

Query Match 13.2%; Score 350.6; DB 11; Length 559;
Best Local Similarity 76.8%; Pred. No. 9.8e-76;
Matches 428; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 1093 actggagatcatgttggtttatctgctgagaactgcgataaactgtcaggaagcagg 1152

Db 2 ATTGGCACACAGTCGGTCTATGCTGATAACTGCACAGAACTGTTGAAGAAGCTGGG 61

QY 1153 aagctgttggttcaacccctggatttctgttttcaattcacacgataaagaacagg 1212

Db 62 AGTTGTTGGGTCAGAAATTTAGATCTATTGTTTCTTTCACACGATTAAGGAGGATGTC 121

QY 1213 tcaccacggaggagctcattaccacacctcttccacaggtccttgcaccttgcagtctgcc 1272

Db 122 ACTTCCCTAGGCGGTTCTCTCCTGCCTCCTTCCCTGGCCCTTGCACTCGGTACTGCA 181

QY 1273 ctgacacgctatgctgatttttgaatctcctcagaaggctctctgattgcttctgcc 1332

Db 182 TTAGCACGCTATGCTGATCTCTTACCCCCACGAAAGGCTGCTTTAGTTGCTTTAGCT 241

QY 1333 gctcatgctctgtaccagtaagaacagagatgcgctttttgtcatcacccttgga 1392

Db 242 GCTCATGCTTCGAACTTAGTAGAAGCAAGAAATTAAGTTCCTTTCATCTCCTCAGGGA 301

QY 1393 aagaatgagattcaaaatgggtagttggaagtcagagagagctttttgagatcatggcc 1452

Db 302 AAGGATGAGTACTCAAAATGGGTGTTGGACCCAGAGAAAGTCTCTTCTGAGGTGATGGCT 361

QY 1453 gagtttccatcagcaaaacccctcttgggtgtgtttttgtgtcagtagcccttcgctta 1512

Db 362 GAGTTCCTCCATCAGCCAAACCTCCCTTGTTGTTTCTGCTAGTCCCTCGTTTA 421

QY 1513 cgcctcgcatactattctatctcatctctcctaaattgctcctcagaattcatgtg 1572

Db 422 CAGCCTCGTTTATTATTCATCTCTCCCTAGGTTCCTCCGAAAGGGTACATGTT 481

QY 1573 acgtgtgcttttagtataatgtaaacccctaccggaaggttcaccagagagtggttcg 1632

Db 482 ACTTGTGCTTGGTGATGTCACACTCCCACTGGTAGAATTCACAAAGGAGTATGTCA 541

QY 1633 acatggatgaagcatgc 1649

Db 542 ACCTGATGAAGAATGC 558

RESULT 8

BF266609

LOCUS

DEFINITION

BF266609 770 bp mRNA EST 09-MAR-2001

DESCRIPTION

HV_CEA0015J11f Hordeum vulgare seedling green leaf EST library

HVCNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone

BF266609

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Hordeum.

REFERENCE

1 (bases 1 to 770)

AUTHORS

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu

, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo

, T., Sasaki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and

Wood, T.

Development of a genetically and physically anchored EST resource

for barley genomics

Unpublished (2000)

On Nov 17, 2000 this sequence version replaced gi:11197604.

COMMENT

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTAACCTCCTCAAGGG

High quality sequence stop: 656.

Location/Qualifiers

1. .770

/organism="Hordeum vulgare"

/cultivar="C116155 (M1a13)"

/db_xref="taxon:4513"

/clone="HV_CEA0015J11f"

/clone_lib="Hordeum vulgare seedling green leaf EST

library HVCNA0004 (Erysiphe infected & control)"

/tissue_type="seedling green leaf"

/lab_host="TJ0121"

/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For

more details on library preparation and sequence analysis

see <http://www.genome.clemson.edu/projects/barley/> To

order a clone see <http://www.genome.clemson.edu/orders>"

BASE COUNT 209 a 150 c 201 g 208 t

ORIGIN

Query Match 13.2%; Score 350.2; DB 11; Length 770;

Best Local Similarity 66.0%; Pred. No. 1.2e-75;

Matches 505; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 455 ttaagtagttgacctggatgactatgacgcagcgagagatcatcaatgagagaattaa 514

Db 3 TCAAAAGTGTGGATCTGGATGACTACTGCTGCCGAGGACGACGAGTACGAGGAGAGCTCA 62


```

RESULT 10
BG444748
LOCUS
DEFINITION
GA_Ea0025H01f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboresum cDNA clone GA_Ea0025H01f, mRNA sequence.
ACCESSION
BG444748
VERSION
BG444748.1 GI:13354400
KEYWORDS
EST.
SOURCE
Gossypium arboreum.
ORGANISM
Gossypium arboreum.
REFERENCE
1. .903
AUTHORS
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL
Unpublished (2000)
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 746.
FEATURES
source
1. .903
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0025H01f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 231 a 197 c 210 g 262 t 3 others
ORIGIN
Query Match 13.0%; Score 343.2; DB 11; Length 903;
Best Local Similarity 67.0%; Pred. No. 6.6e-74;
Matches 508; Conservative 0; Mismatches 235; Indels 15; Gaps 1;
QY 1111 gttatgctgagaactgcgatgaaactgctcgaggaagcagggaagctgttggtcaacc 1170
||||| ||||||| ||||||| ||| ||| ||||||| ||| ||| |||||||
Db 1 GTTACTGTGAGAACCTGGATGAAGTTGTAGATGAAGCATTCAGTTATTGGGCTTATCA 60
QY 1171 ctggattgctgtttcaattcacacggaataaagacggttcacccaggaagctca 1230
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CCAGACACTTATTCTCTATTACACAGATTAAGAGGATGGTACACCATTGGTGAAGT 120
QY 1231 ttacacactctcttccagggttccttgacattacgtatcgtccctagcacgctatgctgat 1290
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TCTTTACCTTCTTCTTCTTCCCTTGTACTTAAGAACAGCAGCTGCGACGATGCTGAT 180
QY 1291 cttttgaactcctcctagaaggctctctctgattgctctgctcgcctatcgtatcctc 1350
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CTTTGTAGCTGCCAAAAGAGCTGCTTACTTGTCTTGGCTGCTCATGCCCTCTGATCCA 240
QY 1351 agtgaagcagagattgctgtttttgtcatcacctctgggaaagaaatagattcaaaa 1410
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 ACTGAAGCCGATCGACTAAGACACCTTGCATCCCTGCTGGAAGATGAGTATGCACAA 300
QY 1411 tgggtagttggaagtcagaggagctcttttggagatcatcgccgagtttccatcagcaaaa 1470
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 TGGATTGTTGCAACACAGAGAAGTCTCCTTGGTTCATGCGGGAATTTCTTCAGCCAG 360

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QY 1471 cccctcttggtgtgttttttctgctgagtagccctcgtcttaccgctcgatactattct 1530
||| ||||||||| ||||||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CCTCCCTCTTGGTGTCTTCTTGCAGCTGTGCTCCAAGGTTGCAGCTAGATATTATCCA 420
QY 1531 atctcatcctcctcaagtgtgctccctcaagaattcatgtgacgtgtgcttagtatat 1590
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ATCTCATCTCCACCAAGGATGGCCACCATCAGGATTCATGTAACCTTGTGCATTGGTTAT 480
QY 1591 ggtcaaaagccctaccggaagggttcaccgaggaggtgtgttcgacatggatgaagcatgca 1650
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 GAGAAACGCCAACAGCTCGTATTACAAAGGTGTTTGTTCAACTTGGATGAAGAATGCT 540
QY 1651 gttcc-----tcaggatagctgggtccctatttttctcgaaagcgtcaaac 1695
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GTGTCTCGGGGAAAACGATGACTGCAGCTGGGACCCCTTTTGTGACGCAATCAAC 600
QY 1696 ttcaagtaccagctgaccctcaactcaattatcatcgtggtgacctggtacaggttta 1755
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 TTAAACTTCCITCAGATATAAAGTGCCTCATCATANTGATTGCTGCTGCTGCTGCTGCTG 660
QY 1756 gctccttcagaggatttctgcaggaaaagatggccctcaagaaaatggtgtcactt 1815
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 GCTCCTTTCAGGGGATTCCTTCAGGAAAGCTTGCACTGAAGAAGCTGGTGTGCTGAGNTG 720
QY 1816 ggccagcagtgctctcttttctcgatgtagaatcgtaa 1853
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 721 GGTCCATCTGTATTGTCTTTGGCTGCAGAACCCGNA 758
RESULT 11
BG450144
LOCUS
DEFINITION
BG450144 580 bp mRNA EST 16-MAR-2001
NF014G11DF1F1088 Drought Medicago truncatula cDNA clone NF014G11DT
5', mRNA sequence.
ACCESSION
BG450144
VERSION
BG450144.1 GI:13368926
KEYWORDS
EST.
SOURCE
barrel medic.
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 680)
AUTHORS
Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
JOURNAL
Unpublished (2000)
COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 680 Std Error: 0.00
Plate: 014 row: G column: 11
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES
Location/Qualifiers
1..680
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF014G11DT"
/clone_lib="Drought"
/tissue_type="plantlets"
/dev_stage="Pooled timepoints"
/notice="Vector: Lambda Zap: Contains a mixture of entire
timepoints."
BASE COUNT 182 a 140 c 156 g 202 t
ORIGIN

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|||||
Db 598 TACACTTG 605

RESULT 13
BG645950
LOCUS
DEFINITION
EST507569 KV3 Medicago truncatula cDNA clone pKV3-48E5 5' end, mRNA
24-APR-2001
ACCESSION
BG645950
VERSION
BG645950.1 GI:13781062
SOURCE
barrel medic.
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 626)
AUTHORS
VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Bowman
,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
TITLE
ESTs from roots of Medicago truncatula 72 h after Rhizobium
inoculation, 2001
JOURNAL
Unpublished (2001)
COMMENT
Contact: VandenBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
M394357e TIGR sequence name: MTECI277K More information is
available at: www.medicago.org
Seq primer: Sknod (CTA gAA CTA gtg gAT CC).
FEATURES
source
Location/Qualifiers
1..626
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-48E5"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
BASE COUNT 165 a 131 c 144 g 186 t
ORIGIN

Query Match 12.6%; Score 333; DB 11; Length 626;
Best Local Similarity 72.6%; Pred. No. 2.1e-71;
Matches 451; Conservative 0; Mismatches 155; Indels 15; Gaps 1;

QY 1492 gctgcagtagccctcgcttaccgctcgtactatctctatctctcctcctaagttt 1551
|||||
Db 1 GCTGCCATAGCCCCCTGTTTACAACTCGTTATTATTCTATTTCATCTCCTTAGTTT 60
QY 1552 gtccctcaagaattcattgctgctgtgtcttagtatatggtcgaagccctaccggaagg 1611
|||||
Db 61 GCCCCACAAAAGGATACACGTAACTTGTGCCCTGGTAGAAGGTCACCACTCCAACCTGCACA 120
QY 1612 gttaaccgaggagtgctgttcgacatggtatgaagcatgcaattcc-----t 1656
|||||
Db 121 ATTCAAAAGGAGGTATGTTCAACCTGGGATCAAGAATGCTATTTCCTCAGAGAAAGCCGT 180
QY 1657 caggatagctgggctcctctattttgttcgaacgtcaaaccttcaagttaccagctgacccc 1716

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|||||
Db 181 GACTGTAGCTGGGCTCCCATTTTATCAGGCCATCGAATTTCAAGCTACCTGCTGATCCT 240
QY 1717 tcaactccaattatcatgtgtggaccctgttacaggggttagctccttcagaggattctg 1776
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Db 241 TCAATTCCTATTATTATGTTGGACCTGGTACTGTTAGCACCTTTTAGGGGATTTTA 300
QY 1777 caggagaagaatggccctcaagaaaaatggtgtcctaacttggcccgagcagtgctcttttc 1836
|||||
Db 301 CAGGAGAGATTGCTCTCAAAGAGAGCGGTGTTCAACTTGGTCTTCATTTACTATTCTTC 360
QY 1837 ggatgtaggaaatcgttaatatggacttcatttatgaagacgaactaaacaacttcgtggaa 1896
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Db 361 GGGTGAGCAACCGCTCAATGGATTTTATATGAGAAAGAGCTGAATAATTGTTGGAA 420
QY 1897 cgaggagtcatttcggagctagttattgctcttttcacgtgaaggggaaagaagaatat 1956
Db 421 CAAGGTTCTCTGTGACAGATTGATAGTTGTCATTCTCTAGAGAGGGCCTGAAAAGGAGTAT 480
QY 1957 gtccaacataagaatgatggagaaagcaacgagatgtatggaatgtgatatacaggggacgtt 2016
|||||
Db 481 GTTCAACACAAATGATGGATAAAGCATCATCTCTGGAGTCTCATTTCTCAGGAAGGT 540
QY 2017 tatctctatgtgtgtgtgatgccaaaggaaatggccagagatgtccatcgcacgttgcat 2076
|||||
Db 541 TATCTTTATGTATGTGTGTCATGCCAAGGCATGCCAGAGATGTTTCATCGAACTCTTCAC 600
QY 2077 accattgccccagaacagggga 2097
Db 601 ACCATTGTCAGCAGCAGGAA 621

RESULT 14
BI424233
LOCUS
DEFINITION
sah67d01.y1 Gm-cl049 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl049-3242 5', similar to SW:NCPR_PHAU0 P37116
NAUPH-CYTOCHROME P450 REDUCTASE ;, mRNA sequence.
ACCESSION
BI424233
VERSION
BI424233.1 GI:15200214
KEYWORDS
EST.
SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 528)
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Boll,B., Marra,M., Hillier,L., Kucaba,F., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Willson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 426.
Location/Qualifiers
1..528
/organism="Glycine max"
/db_xref="taxon:3847"
FEATURES
source

```

```
/clone="GENOME SYSTEMS CLONE ID: Gm-cl049-3242"
/clone_lib="Gm-cl049"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Slecht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."
BASE COUNT      116 a      128 c      120 g      164 t
ORIGIN

Query Match      12.3%; Score 325.6; DB 11; Length 528;
Best Local Similarity 76.3%; Pred. No. 1.4e-69;
Matches 400.; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy 1132 gaactgtcgaggagcaggaagctgttgggtcaacccctggattgctgtttcaatt 1191
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Db 2 GAACACTGTTGAAGAACCTGGGAAGTGTGTTGGTCAGAAATTTAGATCTATTGTTGTTCTCTT 61

Qy 1192 cacacggataaagagcaggggtccaccaggaagctcttaccacctctcttccaggt 1251
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Db 62 CACACTGATAAGGAGGATGGCACTTCCCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121

Qy 1252 ccttgacacttacgatctgcctcagcagcgtatgctgactcttttgaaacctcctagaag 1311
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Db 122 CTTTGCACACTCGCTACTGTCATTTAGCAGCTATGCTGATCTCTTTGAACCCGCCAGAAAG 181

Qy 1312 gctctctgattgctctgtcgcctcatgctctgtaccagtgatgagcagagagattgagc 1371
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Db 182 GCTGCTTTAGTGTCTTTAGCTTCTCATGCTCATGCACTGAACCTAGCAGGAAGATTAAAG 241

Qy 1372 tttttgtcatcacctctctgggaagaatgagttatcaaaatgggtagttggaagtcagagg 1431
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Qy 1552 gctcctcaagaattcatgtgacgtgctttagtatatgctcaaaagcctaccggaag 1611
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Qy 1612 gttaccagagagtggttgcacatgcatggaagcagtcagttcc 1655
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Db 482 ATTCAAAAGGAGTATGTTTCAACCTGGATGAAGAATGCTATTTC 525

RESULT 15
BE461594 590 bp mRNA EST 18-MAY-2001
LOCUS EST413013 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
DEFINITION clone cLEG3966, mRNA sequence.
ACCESSION BE461594
VERSION BE461594.1 GI:9505896
KEYWORDS EST.
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tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 590)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
Unpublished (2000)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..590
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG3966"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_host="breaker"
/lab_host="SOLR"
/notes="Vector: pBluescriptSKmCvadapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT      164 a      111 c      153 g      161 t      1 others
ORIGIN

Query Match      12.3%; Score 325; DB 10; Length 590;
Best Local Similarity 73.1%; Pred. No. 2e-69;
Matches 431.; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 537 catggttagccacttatggtgtagcccaactgacaaatgctgcgagattttcaaatg 596
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Db 1 CATGCTGGCAACTTACGGGGATGGAGAGCAACTGATAATGCTGCAAGGTTTTCACAAATG 60

Qy 597 gttcactcaggaaacatgaaagggagagtggtcttcagcaactaaacttatggtgttttgg 656
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GTTCACTGAGGGACAAGAACGGGTGTCATGTTGCAGAACCTTAGCTATGGCGTTTTTTC 120

Qy 657 tttgggtaaccgtcaatacagcagcatttcaacaagatcgcggtagatggtgagagcaact 716
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Qy 717 cggtaacaagtgtaaacagcattgttcaagtggtgggctcggtgacgatgatcaatgcat 776
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Db 181 GAGTGAACAAGGTCAAAACGCTTGTGGCTTGTGGCTTGTGATGATGATCAGTGCAT 240

Qy 777 tgaagatgattttactgcttgccgagaaattgttgagactgaattgagtcagttgctcaa 836
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Db 241 TGAAGATGATTTTCTGCTGGCCGAGAACAGCTGTGGCCAGAAATTTGGAATCAAAATCTTCTAG 300

Qy 837 agatgagagatgctcctcctcagtggtcacacggtatattgtctactgttctcgaatacag 896
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Db 301 AGACGAGGATGATGAATTTCTGCTGCCACTCCATATACAGCTGCAATTTCTGATATCG 360

Qy 897 ggtagtattcacgaacacggtcgcggtcctggtatgataaacaacataaatactgtctaa 956
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 TTTGGTTATCCATGATACCACTAT--GAGTCTTGAGGATGAAGCATGCAGGCATGGCTAA 417

Qy 957 cygcgatgttgcattttgatattctccatctctgcagaaaccttgttgcctcaacaagaga 1016
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Db 418 TGGGAATACCACATATGATATCCACCACCCCATGCAAGTCAATGTGGCTGTTTCAGAGAGA 477
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Qy 1017 gctccacaaacccaagtctgatatagatcctgtatatacatctgaagttcgaatatcaggctc 1076
Db 478 GCTTCACACACCCGAGTCTGATCGCTCATGTATATACACTTGGAGTTTGATATATCTGGCAC 537
Qy 1077 ttcccttacatatgagactggagatcatgttggtgtttatgctgagaact 1126
Db 538 TGGGATTTCTTATGAACACANGAGATCATGTGGTGTCTTATGCTGAAATTT 587

Search completed: December 27, 2001, 13:07:42
Job time: 2352 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	91.6	3.5	3701	1	US-08-553-279-1	Sequence 1, Appli
2	72.8	2.7	3259	4	US-09-318-448-23	Sequence 23, Appl
3	65.6	2.5	307	4	US-09-172-711-24	Sequence 24, Appl
4	64.2	2.4	5057	2	US-08-365-486A-12	Sequence 12, Appl
5	64.2	2.4	5057	4	US-08-880-342-12	Sequence 12, Appl
6	64.2	2.4	5108	1	US-07-642-002-1	Sequence 1, Appli
7	60.8	2.3	4089	1	US-07-908-245-1	Sequence 1, Appli
8	59.2	2.2	4097	3	US-09-123-708-5	Sequence 5, Appli
9	59.2	2.2	4097	3	US-09-123-624-5	Sequence 5, Appli
10	55.4	2.1	4353	2	US-08-365-486A-18	Sequence 18, Appl
11	55.4	2.1	4353	4	US-08-880-342-18	Sequence 18, Appl
12	55.4	2.1	4780	2	US-08-365-486A-20	Sequence 20, Appl
13	55.4	2.1	4780	3	US-09-123-708-3	Sequence 3, Appli
14	55.4	2.1	4780	3	US-09-123-624-3	Sequence 3, Appli
15	55.4	2.1	4780	1	US-08-880-342-20	Sequence 20, Appl
16	54.2	2.0	4041	1	US-08-147-812-4	Sequence 4, Appli
17	54.2	2.0	4110	3	US-09-123-708-1	Sequence 1, Appli
18	54.2	2.0	4110	3	US-09-123-624-1	Sequence 1, Appli
19	54.2	2.0	4165	1	US-08-147-812-6	Sequence 6, Appli
20	52.2	2.0	7218	1	US-08-232-463-14	Sequence 14, Appl
21	49	1.8	286	4	US-09-172-108-24	Sequence 24, Appl
22	49	1.8	286	4	US-09-172-711-21	Sequence 21, Appl
23	42.6	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl
24	41.4	1.6	4062	4	US-09-126-109-11	Sequence 11, Appl
25	41	1.5	3095	6	5231168-1	Patent No. 5231168
26	39.6	1.5	51259	3	US-08-781-891-209	Sequence 209, Appl
27	39	1.5	2277	1	US-08-676-967-2	Sequence 2, Appli


```

: REGISTRATION NUMBER: 38,615
: REFERENCE/DOCKET NUMBER: 8255-0018
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5057 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: rat bNOS cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 349..4638
: US-08-365-486A-12

Query Match          2.4%; Score 64.2; DB 2: Length 5057;
Best Local Similarity 47.0%; Pred. No. 3.9e-08;
Matches 306; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

QY 1349 ccagtgaagcagagagattgcgtctttttgtcatcactctctggaaagaatgagtattcaa 1408
Db 3698 CTAATCAGAAAGAGAGACGCGGTTCTGCTCTCAGCAAGGGCTCCAGGAATATGAGG 3757

QY 1409 aatggtagttggaatcgagagagtccttttggagatcatgcccaggtttccatcgcaa 1468
Db 3758 AGTGGAAAGTGGGCAAGAACCCACCAATGTTGGAGGTGCTGGAGGAGTTCCCGTCCATCC 3817

QY 1469 aacccctcttggtagtcttcttggtagtagcctcctgcttaccgcctcgatactatt 1528
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QY 1529 ctatctcatctctctcttaagattgtctctcctcaagaattcattgtagcgtgtgctttagtat 1588
Db 3875 CCATCAGCTCTCTCCAGACATGTACCCCGACGAGGTGTCACCTCCTGTTGGCCATGCTCT 3934

QY 1589 atggtcaaaagccctacc-----ggaaggggttcaccgagagtggtgttgcacatgtagta 1642
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QY 1643 agcatcgattctctcagtagctgggtcctctatttttttgcgaacgtcaaaacttcaagt 1702
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QY 1703 taccagctgacccctcaactcccaattatcatggtgggacctggtacaggttagctcctt 1762
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QY 1940 gggaaagaaggaataatgttcaacataagaatgatggagaaagaacacggatg 1990
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RESULT 5
US-08-880-342-12
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: Sequence 12, Application US/08880342
: Patent No. 6218179
: GENERAL INFORMATION:
: APPLICANT: Webster, Keith A.
: APPLICANT: Bishopric, Nanette H.
: APPLICANT: Murphy, Brian
: APPLICANT: Laderoute, Keith R.
: APPLICANT: Green, Christopher J.
: TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/880,342
: FILING DATE: 23-JUN-1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/IB95/00996
: FILING DATE: 13-NOV-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/365,486
: FILING DATE: 23-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Sholtz, Charles K.
: REGISTRATION NUMBER: 38,615
: REFERENCE/DOCKET NUMBER: 8255-0018.30
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5057 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: rat bNOS cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 349..4638
: US-08-880-342-12
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Query Match          2.4%; Score 64.2; DB 4: Length 5057;
Best Local Similarity 47.0%; Pred. No. 3.9e-08;
Matches 306; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

QY 1349 ccagtgaagcagagagattgcgtctttttgtcatcactctctggaaagaatgagtattcaa 1408
Db 3698 CTAATCAGAAAGAGAGACGCGGTTCTGCTCTCAGCAAGGGCTCCAGGAATATGAGG 3757

QY 1409 aatggtagttggaatcgagagagtccttttggagatcatgcccaggtttccatcgcaa 1468
Db 3758 AGTGGAAAGTGGGCAAGAACCCACCAATGTTGGAGGTGCTGGAGGAGTTCCCGTCCATCC 3817

QY 1469 aacccctcttggtagtcttcttggtagtagcctcctgcttaccgcctcgatactatt 1528
Db 3818 AGATGCCGGCTACACTTCTCTCCTCAGCTGTGCGTGC---TGCAGCCTCGCTACTACT 3874
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QY 1529 ctatctcattctctcctaagttgttctccctcaagaattcatgtgacgtgtgtcttttagtat 1588
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QY 1643 agcatgcagttctcagatagctgggtccctatttttttgcgaactcaaaacttcaagt 1702
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RESULT 6

US-07-642-002-1
; Sequence 1, Application US/07642002
; Patent No. 5268465
; GENERAL INFORMATION:
; APPLICANT: Bredt, David S.
; APPLICANT: Hwang, Paul M.
; APPLICANT: Reed, Randall
; APPLICANT: Snyder, Solomon H.
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: One Thomas Circle, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,002
; FILING DATE: 19910118
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kegan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.033576
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 296-5500
; TELEFAX: (202) 296-7830
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5108 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 400...4686
; OTHER INFORMATION:
; US-07-642-002-1

Query Match 2.4%; Score 64.2; DB 1; Length 5108;
Best Local Similarity 47.0%; Pred. No. 3.9e-08;
Matches 306; Conservative 0; Mismatches 333; Indels 12; Gaps 3;
QY 1349 ccagtggaacgagagatgtcgctttttgtcatcactctctgggaagaatgagatttcaa 1408
Db 3749 CTAATGAGAAAGAGAGACGCGGTTGCTGTCTCAGCAAGGGCTCCAGGAATATGAGG 3808
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Db 3809 AGTGAAGTGGGCAAGAACCCCAATGTTGGAGGTGCTGGAGGAGTTCCTCCGTCCATCC 3868
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Db 3869 AGATGCGCGGTACACTTCTCTCCTCAGCTGTCGCTGC---TGCAGCCCTCGCTACTACT 3925
QY 1529 ctatctcattctctcctaagttgttctcctcaagaattcatgtgacgtgtgtcttttagtat 1588
Db 3926 CCATCAGCTCCTCTCCAGACATGTACCCCGACGAGGTGCACCTCACTGTGGCCATCGTCT 3985
QY 1589 atggtcaagccctacc-----ggaagggttccaccgagaggtgtgttcgacatggatga 1642
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QY 1643 agcatgcagttctcagatagctgggtcctctatttttgcgaacttcaaaacttcaagt 1702
Db 4046 ACAGAATACAGGCTGACGATGTAGTCCCTGTCTGTGAGAGTGGCCCTAGCTTCCACC 4105
QY 1703 taccagctgaccctcaactccaattatcatgtgtggacctgtacaggttttagctcctt 1762
Db 4106 TGCCTCGAAACCCCGAGGTCCTTGCATCTCTGGTTGGCCCGAGCAGCTGGCATCGCACCT 4165
QY 1763 tcagagatt---tctgcaggaaagaatggccctcaaggaaaaalgtgtcctcaacttggcc 1819
Db 4166 TCGGAAGCTTCTGGCAACACGCGACAATTTGACATCCAAACACAAAGGAATGAATCCGTGCC 4225
QY 1820 cagcagctcttttccgatgtaggaatcgtaatatggaacttcatttatgaagacgaac 1879
Db 4226 CCATGTTCTGGTCTTCGGGTGTGCAATCCAAAGATAGATCATATCTACAGAGAGGAGA 4285
QY 1880 taacaactctgtggaacgagaggtcatttcgagagtagtttcgagtagttattgctctttcaggaag 1939
Db 4286 CCTCGAGGCTAAGAAACAAAGGGCGTCTTCAGAGAGGTGTACACTGTCTATTTCCTGGGAAC 4345
QY 1940 gggaaaaagaagaataatgttcaacataagatgatggagaagaacacggatg 1990
Db 4346 CGGACAGCCARAGAAATATGTACAGGACCTGCTGCAGGACAGCTGGCTG 4396

RESULT 7

US-07-908-245-1
; Sequence 1, Application US/07908245
; Patent No. 5498539
; GENERAL INFORMATION:
; APPLICANT: Harrison, David G.
; APPLICANT: Alexander, R. Wayne
; APPLICANT: Murphy, T.J.
; APPLICANT: Nishida, Ken'ichi
; TITLE OF INVENTION: Endothelial Nitric Oxide Synthase


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Query Match          2.2%; Score 59.2; DB 3; Length 4097;
Best Local Similarity 50.6%; Pred. No. 9.1e-07;
Matches 170; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

QY 1613 ttcaccgagagtggtttgacatgagatgaagcagtcagttcttcacgagtagctggctc 1672
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Db 2975 tacactacgggtctgtctccacatggtcagtcagcagtcgaagactggagaccgcgtccct 3034

QY 1673 ctatttttttgcgaacgtcaaaacttcaagtattaccagctgaccctcacaactcaattatca 1732
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3035 gcttcacagggggtccctctccctccgctgcccgcctgacccctacgtgcctgcaccc 3094

QY 1733 tsgtgggaacctggtacaggttagctctcttcagaggtatttcgacgaaagaatg---g 1789
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Db 3095 tegtgggacctggcactggcctccctccctccggtgatttggcaggagagcgtgcacg 3154

QY 1790 cctcaagaaagtgtgctcaacttggcccagcagtgctctcttttcgagtaggaatc 1849
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3155 acatggagagaaaaggctgcagcgcaccccatgacctggtgttcggctgccctgct 3214

QY 1850 gtaatatggaactctatttatgaagcagaactaaacaacttcgtggaacgagagtgatctt 1909
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3215 cccaaactcgacatctctaccgcgacgaggtgcaggacgcccagggcggtgttg 3274

QY 1910 cggagctagttatgctcttttcacgtgaagggaagaa 1945
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Db 3275 gccggtctccaccgctctctcccggaacctgaca 3310

RESULT 10
US-08-365-486A-18
; Sequence 18, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365.486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4353 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al.,
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4305
US-08-365-486A-18

Query Match          2.1%; Score 55.4; DB 2; Length 4353;
Best Local Similarity 46.8%; Pred. No. 1.1e-05;
Matches 284; Conservative 0; Mismatches 311; Indels 12; Gaps 3;

QY 1349 ccagtgaaagcagagattgcgtttttgtcatccactctgggaaagaatgatttcaaa 1408
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Db 3365 CCAGCGAGAGAGAGAGACGCGTCTGCTGCTTCAGCAGAGGTTTTCAGGAGTAGCAGG 3424

QY 1409 aatgggtagttggaagtcagaggagtccttttgagatcatgcccaggtttccatcagcaa 1468
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Db 3425 AATGGAAATGGGGCAGAACCCACCACATCGTGGAGGTGCTGGAGGAGTTCCCATCTATCC 3484

QY 1469 aacccctcttgggtgttttcttgcagtagtgcctcgcctgcctaccgcctcgatactatt 1528
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Db 3485 AGATGCGCGCCACCCCTGCTCTGACCCAGCTGTCCCTGC---TGCAGCCCCGCTACTATT 3541

QY 1529 ctatctcatctctcctaaagtgttgcctcctcaagaattcatgtgacgtgtgttttagtat 1588
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3542 CCATCAGCTCTCCCCAGACATGTACCCTGTAGTGAAGTGGACCTCACTGTGGCCATCGTTT 3601

QY 1589 atggtcaaaagcctaccggaagg-----ttcacccgaggagtggttcgacatggatga 1642
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3602 CCTACCGCACTCGAGATGGAGAAGGACCAATTACACCACGGCGTATGCTCCTCTGGCTCA 3661

QY 1643 agcatgagttctcctcaggtatagctgggtcctctatttttgcgaaacgtcaaaccttcaagt 1702
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3662 ACCGGATACAGGCTGACGAACCTGTCCTCCCTGTTTCTGTGAGAGGAGCACCGCTTCACC 3721

QY 1703 taccagctgacccctcaactccaattatcatgtggagacctggtacaggttagctccct 1762
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Db 3722 TGCCCCGGAACCCCAAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3781

QY 1763 tcagagagattctgcaggaaag---aatggccctcgaagaaatgctcgaacttggcc 1819
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3782 TCCGAAGCTTCTGGCAACAGCGGCAATTTGATATCCACACAAGGAATGAACCCCTGCC 3841

QY 1820 cagcagtgctcttttcggatgtagaatcgtaataatgacttcatttatgaagcgaac 1879
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3842 CCATGGTCTCTGCTTCTCGGGTGCCGCAATCCAAGATAGATCATATCTACAGGGAAGAGA 3901

QY 1880 taacaacttcgtggaacgagagtcatttcggagctagtagtattgcttttcacgtgaag 1939
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3902 CCTGTGAGGCCCAAGAACAAAGGGGCTCTTCAGAGAGCTGTACAGGCTTACTCCCGGAGC 3961

QY 1940 gggaaaaa 1946
      |||||
Db 3962 CAGACAA 3968

RESULT 11
US-08-880-342-18
; Sequence 18, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
```

```
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880.342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al.
INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4305
US-08-880-342-18

Query Match 2.1%; Score 55.4; DB 4; Length 4353;
Best Local Similarity 46.8%; Pred. No. 1.1e-05;
Matches 284; Conservative 0; Mismatches 311; Indels 12; Gaps 3;

QY 1349 ccagtgaagcagagagattgcgctttttgtcatcaccctctgggaagaatgagattcaaa 1408
DB 3365 CCAGCGAAGGAGAGAGAGCGCTGCTGCTCTAGCAGAGGTTTGCAGGAGTAGCAGG 3424
QY 1409 aatgggtagttggaagtcagagagagtccttttgagatcatatggccgaggtttccatcagcaa 1468
DB 3425 AATGGAATGGGGCAAGAACCCACCACCTCGTGGAGGTGCTGGAGGAGTCCCATCTATCC 3484
QY 1469 aacccctcttggtgtgttctttgtgagtagcagccctgcctaccgcctcgatactatt 1528
DB 3485 AGATGCCGCCACCCCTGCTCTGACCCAGCTGCTCCCTGTC---TGCAGCCCGCTACTATT 3541
QY 1529 ctatctcatctctcttaagtgtgtctccctcaagaattcatgtgacgtgtgctttagtat 1588
DB 3542 CCATCAGCTCTCTCCCGAGACATGTACCTGTAGTAGAGTGACCTCACTGTGGCCATCGTTT 3601
QY 1589 atggtcaagccctaccggaaggg-----ttcacaggagagtggttttcgacatgatga 1642
DB 3602 CCTACCGCACTCGAGATGGAGAGGACCAATTCACCACGCGGTATGCTCTCTCGCTCA 3661
QY 1643 agcatgcagttctcaggtagctggtgtctctatttttttgcgaagctcaaaactcaagt 1702
DB 3662 ACCGGATACAGGCTGACGAAGTGGTCCCTGTTCTGTGAGAGGAGCACCAAGCTTCCACC 3721

QY 1703 taccagctgaccctccaactccaattatcatcattggtgggaacctggtacagaggttagctcctt 1762
DB 3722 TGCCCGGAACCCCAAGTCCCTGTCATCTCTGTTGACGACGACCGCATTTGCCCTT 3781
QY 1763 tcagaggtttctgcaggaag--aatgcccctcaaggaataatggtcctaacttggcc 1819
DB 3782 TCCGAAGCTTCTGGCAACAGCGGCAATTGTATATCCAAACACAAGGAATGAACCCCTGCC 3841
QY 1820 cagcagtgctcttttttcggatgtaggaatcglaatatggacttcatttatgaagacgaac 1879
DB 3842 CCATGCTCTCTGCTCTCTCGGGTCCCGCAATCCAAGATAGATCATATCTACAGGGAAGAGA 3901
QY 1880 taacaacattcgtgaacagagagtcatttcgagagtagttattgctcttttcacgtgaag 1939
DB 3902 CCTGCAGGCCAAGAACAAAGGGGGTCTTCAGAGAGGTGTACACGGCTTACTCCCGGAGC 3961
QY 1940 gggaaaa 1946
DB 3962 CAGACAA 3968

RESULT 12
US-08-365-486A-20
; Sequence 20, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human NOS-SN gene, Nakane, et al.
; INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 431..4732
; US-08-365-486A-20

Query Match 2.1%; Score 55.4; DB 2; Length 4780;
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	Best Local Similarity	46.8%	Pred. No. 1.2e-05;	
	Matches 284;	Conservative 0;	Mismatches 311;	Indels 12; Gaps 3
Qy	1349	ccagtgaagcagagagattgcgcttttggctcatcacctctgggaagaatcagattatcaa	1408	
Db	3792	CCAGGAGAGGAGAAAGCAGCGTCTGCTGGTCTCTAGCAAGGGTTTGAGGAGTACGAG	3851	
Qy	1409	aatgggtagttgggaagtcagagagagcttttggagatcatcgccgagtttccatcagcaa	1468	
Db	3852	AATGAAATGGGCAAGAACCCACCATCGTGGAGGTCTGGAGGAGTCCCATCTATCC	3911	
Qy	1469	aacccctctctggtgtgttttcttctgctgagtagccccctcgctttaccgctcgatactatt	1528	
Db	3912	AGATGCCGGCCACCTGCTCTGTGACCCAGCTGTCCCTGC--TGCAGCCCGCTACTATT	3968	
Qy	1529	ctatctcatctctcttaagtttgcctcctcaagaattcatgtgacgtgtgtcttagtat	1588	
Db	3969	CCATAGCTCTCCCCAGACATGTACCCCTGATGAGTGCACCTCACTGTGCCCATCGTTT	4028	
Qy	1589	atggttcaaaagccctaccggaagg-----ttcacaggaggagtgtgttcgacatgatga	1642	
Db	4029	CCTACCGCACTCGAGATGGAGAGAGACCAATTCAACACGGCGTATGCTCTCTCTGSGCTCA	4088	
Qy	1643	agcatgcagttcttcacgagatagctgggctcctattttgttcgaacgttcaaacctcaagt	1702	
Db	4089	ACCGGATACAGGCTGACGAACATGGTCCCTCTTTCTGTGAGAGGACACCCAGCTTCCACC	4148	
Qy	1703	taccagctgacccctcaactccaattatcatggtgggacctggtcacaggttagctcctt	1762	
Db	4149	TGCCCGGAAACCCCAAGTCCCTCTGTCATCTCTGTTGGACACGACCCGGCAATGCCCCCT	4208	
Qy	1763	tcagagagattctgcaggaag---aatggccctcaaggaataatggtctcaacttggcc	1819	
Db	4209	TCCGAAGCTTCTGGCAACACGCGCAATTGTGATATCCAAACAAAGGAATGAACCCCTGCC	4268	
Qy	1820	cagcagtgctcttttccgatatgtaggaatcgaatataggaactcatttatgaagacgaac	1879	
Db	4269	CCATGGTCTCTGGTCTTCGGGTGCCGGCAATCCAGATAGATCATATCTACAGGGAAGAGA	4328	
Qy	1880	taacaactctgtggaacgagagagtcattctcgagctagttatgctcttttccagtgag	1939	
Db	4329	CCCTGCCAGGCCAAGAACAAAGGGGTCTTCAGAGAGCTGTACACGGCTTACTCCCGGGAGC	4388	
Qy	1940	gggaaaa	1946	
Db	4389	CAGACAA	4395	

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RESULT 13
US-09-123-708-3
; Sequence 3, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4780
; TYPE: DNA
; ORGANISM: Cytomegalovirus
US-09-123-708-3

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Query Match				2.1%;	Score 55.4;	DB 3;	Length 4780;
Best Local Similarity				46.8%;	Pred. No. 1.2e-05;		
Matches 284;				Conservative	0;	Mismatches 311;	Indels 12; Gaps 3
Qy	1349	ccagtgaagcagagagattgcgctttttgtcatcacccttgggaagaatgagtattca	1408				
Db	3792	ccagcgaaaggaagcagcgctgcgtgctcagcaagggtttgcaggagtcagagg	3851				
Qy	1409	aatgggtagttggaaagtcagagagatcttttggagatcatgcccgcagttccatcagcaa	1468				
Db	3852	aatggaaatgggcaagaccaccacgcgtggaggtgctggagagttcccatctatcc	3911				
Qy	1469	aacccctcttgggtgtgttttggtcgagtagccctcgtctaacgcctcgatactatt	1528				
Db	3912	agatgcggccacccctgcctcagcccagctgcctcgc---tgagccgcgcctactatt	3968				
Qy	1529	ctatctcatctctctcaagtttgcctcctcaagaattcatgtgacgtgcttttagtat	1588				
Db	3969	ccatcagctctctcccaagacatgtacctcgtgatgaagtcacctcactgtgcccacgtttt	4028				
Qy	1589	atggtcaaaagccctaccocggaaaggg-----ttcacaggagagtgctgttcgacatggatga	1642				
Db	4029	octaccgcactcagatggagaagaccaaattcacccagcgctatgctcctcctggtctca	4088				
Qy	1643	agcatgcagttcttcagatagctgggtccctatttttgttcgaagtcctaaactcaagt	1702				
Db	4089	accggatcacaggtgcagcaactggtccctgttctgtagagaggacaccacgcttccacc	4148				
Qy	1703	taccagctgacccctcaactccaattatcatggtgggacctggtacagaggttagctcctt	1762				
Db	4149	tgcccggaaaccccaagtccctcgtcatcctcgttggaccaggccacggcattgcccctt	4208				
Qy	1763	tcagagatttctcagaaaag---aatggccctcaaggaaaataggtctcaacttgccc	1819				
Db	4209	tccgaagctcttggcaacagcggcaatttgatctccacacaaaaggaaatgaacccctgcc	4268				
Qy	1820	cagcagtgctcttttcggatgtaggaatcgtaatatggacttcatttatgaagcagcaac	1879				
Db	4269	cca1ggtcctggtcttcgggtgcgcggcaatccaagatagatcatatctacagggaagaga	4328				
Qy	1880	taacaactctgtggaacgagagatcattctcggaactagttattgccctttcaactggaag	1939				
Db	4329	ccctgcagggccaaagaacaaaggggtcttcagagagcgttacacggcttactccccggagc	4388				
Qy	1940	ggggaaaa	1946				
Db	4389	cagacaa	4395				

RESULT 14
US-09-123-624-3
; Sequence 3, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Jurgen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4780
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-123-624-3

	Query Match	2.18;	Score 55.4;	DB 3;	Length 4780;
	Best Local Similarity	46.8%;	Pred. No. 1.2e-05;		
	Matches 284;	Conservative 0;	Mismatches 311;	Indels 12;	Gaps 3;
Qy	1349	ccagtgaagcagagagattgcgcttttggatcatcacctctgggaagaagatgagtattcaaa	1408		
Db	3792	ccagcgagaaggagacgacgcgtctgctggtccctcagcaagggitttcagagagtagcagg	3851		
Qy	1409	aatgggtagttgggaagtcagagggagtgcttttggagatcatgcccaggtttccatcagcaa	1468		
Db	3852	aatggaaatggggcaagaaccaccaactcgtyggagtgctggagaggttcccatatccc	3911		
Qy	1469	aacctcttgggtgttcttctgctgagtagccccctgcgtcttacccgctcgatactatt	1528		
Db	3912	agatgccggccaccctgctcctgaccacgcgtgctccctgc----	3968		
Qy	1529	ctattctatcctctccaagtttgtctcctcacaagaattcatgtgacgtgctgttttagtat	1588		
Db	3969	ccatcagctctcccagacatgtacctgtgatgaagtgcacctcaactgtgcccacgtttt	4028		
Qy	1589	atggtcaaacgcctaccgggaagg;-----ttaccaggaggagtgtgttcgacatggatga	1642		
Db	4029	cctaccgcactcgagatggagaaggaccaatctcacacggcgatgtgctcctctgggtcca	4088		
Qy	1643	agcatgcagttctctcaggaatagctgggctcctatttttgttcgaacgtccaactccaagt	1702		
Db	4089	accggatatcaggctgcagcaactgtctccctgttctgtgagaggagcacccagcttccacc	4148		
Qy	1703	taccagctgcacctcaactcaattatcatggtgggacctggttacagggttagctcctt	1762		
Db	4149	tgcctggaaaccccccaagctccctcgatcctcgttggaccaggcacccggcatgtccctt	4208		
Qy	1763	tcagaggatttctcaggaagaag---aatggccctcaaggaaaattggtgctcaacttgccc	1819		
Db	4209	tcogaactcttgccaacagcgcgcaatttgatatccaacacaaaggaatgaacctctgcc	4268		
Qy	1820	cagcagtgctcttttctcggaatgtaggaatcgtaatatgtgaacttcatatgaagacgaac	1879		
Db	4269	ccatggtctctggtcttcgggtgcgcggcaatccaagatagatcatactcacagggaagaga	4328		
Qy	1880	taaacaacttcgtggaaacgagaggtcatttctcgagactagttattgccttttcaactggaag	1939		
Db	4329	ccctgcaggccaagaacaagggggtcttctcagagagctgtacacggcttactccccgggagc	4388		
Qy	1940	gggaaaa	1946		
Db	4389	cadacaa	4395		

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RESULT 15
US-08-880-342-20
; Sequence 20, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/880.342
 FILING DATE: 23-JUN-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/IB95/00996
 FILING DATE: 13-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/365.486
 FILING DATE: 23-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38.615
 REFERENCE/DOCKET NUMBER: 8255-0018.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4780 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human NOS-SN gene, Nakane, et al.
 INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 431..4732
 US-08-880.342-20

Query Match	2.1%	Score 55.4	DB 4	Length 4780
Best Local Similarity	46.8%	Pred. NO. 1.2e-05		
Matches 284	Conservative	0	Mismatches 311	Indels 12
Gaps				
Qy 1349	ccagtgaaagcagagagattgcgcttttggatcatcactctctgggaaagaatgagtattcaa	1408		
Db 3792	CCAGCCGGAAGAGAGACGCTGCTGCTGCTCCTCAGCAAGGGTTTGCAGAGTACGAGG	3851		
Qy 1409	aatgggttagtggaaagtcagagaggtcttttggagatcatggcgcgagtttccatcagcaa	1468		
Db 3952	ANTGGAAATGGGCGACAGACCCACCATCGTGGAGGTGCTGGAGAGGTTCCCATCTTATCC	3911		
Qy 1469	aacccctcttgggtgtgttcttttgcagtagccccctcgcttaccgcctcgatactatt	1528		
Db 3912	AGATGCGCGCCACCTTGCTCTGACCCAGCTGTGCTCCTGCG--TGCAGCCCGCTACTATT	3968		
Qy 1529	ctatctcatctctctctaagtttgbtccctcaagaattcatgtgacgtggtctttagtat	1588		
Db 3969	CCATCAGCTCTCTCCCGACATGTACCTGTATGAAGTGCACCTCACTGTGGCCATCGTTT	4028		
Qy 1589	atggtcaagccctaacggaaagg-----ttcacccaggagtggtgttcgcacatgtagta	1642		
Db 4029	CCTACCGCACTCGAGATGGAGAAGGACCAATTTTTCACCGGGCGTATGCTCTCTGGGTCA	4088		
Qy 1643	agcatgcagttctcaggtagctgggtccctatttttgcgaacgttcaaaccttcaagt	1702		
Db 4089	ACCGGATACAGGCTGACGAACCTTGCTTCCCTGTTTTCGTGAGAGGAGCACCAGCTTCCACC	4148		
Qy 1703	taccagctgaccctcaactccaattatcatggtgggacctgggtacagggttagctcctt	1762		
Db 4149	TGCCCCGAACCCCCAAGTCCCTGTCATCTCTGTTGGACAGGCACCGGCATTGCCCTT	4208		
Qy 1763	tcagaggaattctgcaggaaag---aatggccctcaagaaaaatgggtctcaacttggcc	1819		
Db 4209	TCCGAAGCTTCTGGCAACAGCGGCAATTTGATPATCCAACAAAGGAATGAACCCCTGCC	4268		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:28:45 ; Search time 2201.93 Seconds
(without alignments)
12927.553 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcagcttgtagtat.....ttttgagaaaaaaaaaaaaa 2649

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 537289281 residues

Word size : 0
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	1.1	424	10	AV409610
2	29	1.1	675	10	AL505302
3	27	1.0	531	10	AW932267
	26	1.0	415	10	AV539473
c 4	26	1.0	498	10	AV548760
c 5	26	1.0	415	10	AV548760
c 6	26	1.0	536	10	AV546032
c 7	26	1.0	543	10	AI998902
c 8	26	1.0	601	10	AV540686
c 9	26	1.0	624	13	AQ958450
c 10	26	1.0	746	13	AQ958449
c 11	24	0.9	146	10	AW255611
c 12	23	0.9	124	10	AI705252

c 13	23	0.9	215	11	BI283532
c 14	23	0.9	245	10	AI961647
c 15	23	0.9	245	11	BE984614
c 16	23	0.9	268	10	AA669107
c 17	23	0.9	307	10	BE248453
c 18	23	0.9	312	10	AI689639
c 19	23	0.9	375	10	AI843164
c 20	23	0.9	382	11	BE988116
c 21	23	0.9	392	10	AI469773
c 22	23	0.9	402	11	BG557935
c 23	23	0.9	419	11	BG371805
c 24	23	0.9	421	11	BI276373
c 25	23	0.9	427	10	AA493217
c 26	23	0.9	438	11	BG881606
c 27	23	0.9	439	10	AW396232
c 28	23	0.9	441	11	H07123
c 29	23	0.9	456	10	BE203172
c 30	23	0.9	477	10	AL365946
c 31	23	0.9	479	10	AA924768
c 32	23	0.9	485	10	AI850041
c 33	23	0.9	496	10	AW509065
c 34	23	0.9	500	10	AW745723
c 35	23	0.9	509	10	BE057747
c 36	23	0.9	510	10	BE346181
c 37	23	0.9	512	10	AW690487
c 38	23	0.9	517	10	BE608297
c 39	23	0.9	518	11	BF003751
c 40	23	0.9	521	11	BF631848
c 41	23	0.9	526	11	BI425956
c 42	23	0.9	532	10	AW691469
c 43	23	0.9	537	10	BE347704
c 44	23	0.9	538	11	BG241454
c 45	23	0.9	541	11	BG652476

ALIGNMENTS

RESULT 1

AV409610 424 bp mRNA EST 23-MAY-2000
LOCUS AV409610 Lotus japonicus young plants (two-week old) Lotus
DEFINITION japonicus cDNA clone MML060b02_r 5', mRNA sequence.
ACCESSION AV409610
VERSION AV409610.1 GI:7722464
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.

REFERENCE 1 (bases 1 to 424)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamuekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

FEATURES

source
1. 424
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MML060b02_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stages="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; Isolate=Miyakojima MG-20"
99 a 124 c 101 g 100 t

BASE COUNT

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ORIGIN
Query Match      1.1%; Score 29; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 376 ggtaactcagactggtactgctaagatt 404
Db 340 GGTACTCAGACTGGTACTGCTGAAGATT 368

RESULT 2
AL505302
LOCUS      AL505302      675 bp      mRNA      EST      04-JAN-2001
DEFINITION AL505302 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone
            HW08A19V 5', mRNA sequence.
ACCESSION  AL505302
VERSION     AL505302.1 GI:12031517
KEYWORDS   EST.
SOURCE     barley.
ORGANISM   Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 675)
AUTHORS   Michalek W., Weschke W., Pleissner K.-P. and Graner, A.
TITLE     EST sequencing and analysis in barley
JOURNAL   Unpublished (2000)
COMMENT   Contact: Michalek W
            Institute for Plant Genetics and Crop Plant Research
            Corrensstr.3, D-06466 Gatersleben, Germany
            Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
            Seq primer: T3 primer for 5'end.
            Location/Qualifiers
                1..675
                /organism="Hordeum vulgare"
                /cultivar="Barke"
                /db_xref="taxon:4513"
                /clone="HW08A19V"
                /clone_lib="Hordeum vulgare Barke roots"
                /tissue_type="roots"
                /lab_host="XL0LR"
                /note="Vector: plasmid pBK-CMV; Site.1: EcoRI; Site.2:
                XhoI; mRNA was made from roots of spring barley variety
                'Barke', a high quality malting variety. Roots were grown
                for two days on filter paper at room temperature. Cloning
                sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA).
                NOTE: Due to a cloning artefact caused by the kit, in most
                cases the EcoRI site is NOT present, as well as the EcoRI
                adapter. Average insert size is 1 kb. Sequence trimming:
                Vector sequences and sequence ends were trimmed from the
                5'- and 3'-end until a 50 bp window contains less than two
                ambiguities. The maximum length was set to 700 bp"
BASE COUNT  178 a 158 c 164 g 174 t 1 others
ORIGIN

Query Match      1.1%; Score 29; DB 10; Length 675;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 acatagactgagatcatgttgggtg 1112
Db 469 ACATATGACGTGAGATCATGTGGTGT 497

RESULT 3
AW932267
LOCUS      AW932267      531 bp      mRNA      EST      18-MAY-2001
DEFINITION EST358110 tomato fruit mature green, TAMU Lycopersicon esculentum
            cDNA clone cLEF47H10 5', mRNA sequence.
ACCESSION  AW932267

ORIGIN
Version Match      1.0%; Score 27; DB 10; Length 531;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 763 gatgatcaatgcatggaagatgattt 789
Db 224 GATGATCAATGCAATGAGATGATTTT 250

RESULT 4
AV539473/c
LOCUS      AV539473      415 bp      mRNA      EST      07-SEP-2000
DEFINITION AV539473 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
            cDNA clone RZ133e03F 3', mRNA sequence.
ACCESSION  AV539473
VERSION     AV539473.1 GI:8701230
KEYWORDS   EST.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 415)
            Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
            A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
            DNA Res. 7, 175-180 (2000)
JOURNAL    20363093
MEDLINE
COMMENT    Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

```


Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

Location/Qualifiers
1. 415
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 132 a 93 c 67 g 123 t
ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 415;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatgagaa 1979
|||||
Db 412 TATGTTCAACATAAGATGATGAGAA 387

RESULT 5

AV548760/c 498 bp mRNA EST 06-SEP-2000
LOCUS
DEFINITION AV548760 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
cDNA clone RZL61C08F 3', mRNA sequence.

ACCESSION AV548760
VERSION AV548760.1 GI:8720173
KEYWORDS EST.

SOURCE
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 498)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)

20363093
COMMENT

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Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

Location/Qualifiers
1. 498
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 155 a 112 c 82 g 149 t
ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 498;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatgagaa 1979
|||||
Db 423 TATGTTCAACATAAGATGATGAGAA 398

RESULT 6

AV546032/c

LOCUS

DEFINITION AV546032 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
cDNA clone RZL07e01F 3', mRNA sequence.

ACCESSION AV546032
VERSION AV546032.1 GI:8717446
KEYWORDS EST.

SOURCE
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 536)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)

20363093
COMMENT

Contact: Erika Asamizu
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Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

Location/Qualifiers
1. 536
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 170 a 122 c 90 g 154 t
ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 536;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatgagaa 1979
|||||
Db 388 TATGTTCAACATAAGATGATGAGAA 363

RESULT 7

LOCUS

DEFINITION AI996902/c 543 bp mRNA EST 08-SEP-1999
701516529 A. thaliana, Columbia Col-0, root-2 Arabidopsis thaliana
cDNA clone 701516529, mRNA sequence.

ACCESSION AI996902
VERSION AI996902.1 GI:5843807
KEYWORDS EST.

SOURCE
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 543)
Chen, J., Mollman, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
Wang, X., Hillman, J., Guebler, K., Kim, C., Doyle, M., Brzoska, P.,
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,
Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,
Pollock, J., Suzuki, G., Argentine, C., Shah, S., Nobrega, A., Murry, L.,
Turner, C., Krikorian, S., Elder, L. and Hanson, D.

Arabidopsis thaliana Gene Expression MicroArray
Unpublished (1999)
Contact: David Smoller, Ph.D.

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Pharmaceuticals, Inc.
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Tel: 877-577-2733
 Fax: 314-427-3324
 Email: service@genomesystems.com.

FEATURES

source
 1. .543
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia Col-0"
 /db_xref="taxon:3702"
 /clone="701516525"
 /clone_lib="A. thaliana, Columbia Col-0, root-2"
 /tissue_type="root"
 /dev_stage="4 - 7 weeks"
 /note="vector: pSPORT; Site_1: NotI; Site_2: SalI; cDNA library was derived from untreated root tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."
 170 a 126 c 91 g 156 t

BASE COUNT
 ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 543;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatggagaa 1979

Db 380 TATGTTCAACATAGATGATGGAGAA 355

RESULT 8

AV540686/c AV540686 601 bp mRNA EST 06-SEP-2000
 LOCUS AV540686 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
 DEFINITION cDNA clone R2153g03f 3', mRNA sequence.

ACCESSION AV540686

VERSION AV540686

KEYWORDS EST.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 601)
 Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
 DNA Res. 7, 175-180 (2000)

JOURNAL 20363093

MEDLINE

COMMENT Contact: Erika Asamizu

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Kazusa DNA Research Institute

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Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES 1. .601

source /organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/clone="R2153g03f"

/clone_lib="Arabidopsis thaliana roots Columbia"

/tissue_type="roots"

/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

184 a 137 c 97 g 183 t

BASE COUNT

ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 601;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatggagaa 1979

Db 443 TATGTTCAACATAGATGATGGAGAA 418

RESULT 9

AQ958450

LOCUS

DEFINITION

AQ958450

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 624)

AUTHORS

Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.

TITLE

Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms

JOURNAL

COMMENT

Unpublished (2000)

Contact: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: at@tigr.org

For additional information, see http://www.tigr.org/tdb/at/at.html

Seq primer: TR

Class: shotgun.

FEATURES

source

1. .624

/organism="Arabidopsis thaliana"

/strain="Landsberg erecta"

/db_xref="taxon:3702"

/clone="LERAX59"

/clone_lib="LERA"

/note="Organ: Leaf; Vector: PHOS1; Total genomic DNA was sheared to 0.9-1 kbp before ligation."

BASE COUNT 175 a 114 c 134 g 199 t

ORIGIN

Query Match 1.0%; Score 26; DB 13; Length 624;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatggagaa 1979

Db 488 TATGTTCAACATAGATGATGGAGAA 513

RESULT 10

AQ958449/c

LOCUS

DEFINITION

AQ958449

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 746)
REFERENCE
AUTHORS Buell,C.R., Lin,X., Pal,G., Barnstead,M., Bowman,C., Utterbach,T.,
Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
TITLE Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
JOURNAL Unpublished (2000)
COMMENT Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atetigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TF
Class: shotgun.

FEATURES             Location/Qualifiers
     source           1..746
     -organism="Arabidopsis thaliana"
     -strain="Landsberg erecta"
     -db_xref="taxon:3702"
     -clone="LERAX59"
     -clone_lib="LERA"
     /note="Organ: Leaf; Vector: pHS1; Total genomic DNA was
sheared to 0.9-1 kbp before ligation."
BASE COUNT    233 a 180 c 120 g 213 t
ORIGIN
Query Match          1.0%; Score 26; DB 13; Length 746;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatgacaa 1979
|||||
Db 421 TATGTTCAACATAAGATGATGAGAA 396

RESULT 11
AW255611
LOCUS AW255611 146 bp mRNA EST 23-AUG-2000
DEFINITION M1658 peppermint glandular trichome Mentha x piperita cDNA, mRNA
sequence.
ACCESSION AW255611
VERSION AW255611.1 GI:7244863
KEYWORDS EST.
SOURCE peppermint.
ORGANISM Mentha x piperita
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiaceae; Mentha.
1 (bases 1 to 146)
REFERENCE
AUTHORS Lange,B.M., Wildung,M.R., Stauber,E.J., Sanchez,C., Pouchnik,D. and
Croteau,R.
TITLE Probing essential oil biosynthesis and secretion by functional
evaluation of expressed sequence tags from mint glandular trichomes
Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)
20183992
Contact: Lange, B.M.
Institute of Biological Chemistry/Washington State University
Pullman, WA
Email: lange-m@mail.wsu.edu.

FEATURES             Location/Qualifiers
     source           1..146
     -organism="Mentha x piperita"
     -cultivar="Black Mitcham"
     -db_xref="taxon:34256"
     -clone_lib="peppermint glandular trichome"
     /tissue_type="peltate glandular trichomes"
     /cell_type="secretory"
     /note="vector: lambda ZAPII"
BASE COUNT    46 a 33 c 32 g 35 t

```

ORIGIN

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Query Match          0.9%; Score 24; DB 10; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1855 atggacttcattatgaagacgaa 1878
|||||
Db 6 ATGGACTTCATTATGAAGACGAA 29

RESULT 12
AI705252/c
LOCUS AI705252 124 bp mRNA EST 03-JUN-1999
DEFINITION UI-R-AF0-xy-h-09-0-UI.s1 UI-R-AF0 Rattus norvegicus cDNA clone
UI-R-AF0-xy-h-09-0-UI 3', mRNA sequence.
ACCESSION AI705252
VERSION AI705252.1 GI:4993152
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 124)
REFERENCE
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized AV canal at 15 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes.
Location/Qualifiers
     source           1..124
     -organism="Rattus norvegicus"
     -strain="Sprague-Dawley"
     -db_xref="taxon:10116"
     -clone="UI-R-AF0-xy-h-09-0-UI"
     -clone_lib="UI-R-AF0"
     -dev_stage="adult"
     -lab_host="DH10B (Life Technologies)"
     /note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AF0
library is a non-normalized library constructed from 15
dpc rat atrioventricular (AV) canal. The tag is a string
of 5 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_LIB=UI-R-AF0
TAG_TISSUE=AV canal at 15 dpc
TAG_SEQ=GAAGG"
BASE COUNT    21 a 33 c 24 g 46 t
ORIGIN

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Query Match      0.9%; Score 23; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2627 gagtttgagaaaaa 2649
Db 26 GAGTTTTCAGAAAAA 4

RESULT 14
LOCUS AI961647/c 245 bp mRNA EST 09-MAR-2000
DEFINITION wt65C05.x1 NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2512328 3',
mRNA sequence.
ACCESSION AI961647
VERSION AI961647.1 GI:5754360
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1477 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 220.
Location/Qualifiers
1..245
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2512328"
/clone_lib="NCI_CGAP_Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
BASE COUNT 50 a 61 c 63 g 71 t
ORIGIN

Query Match      0.9%; Score 23; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2627 gagtttgagaaaaa 2649
Db 33 GAGTTTTCAGAAAAA 11

RESULT 15
LOCUS BE984614/c 245 bp mRNA EST 05-OCT-2000
DEFINITION UI-M-CG0p-bdf-f-01-0-UI.s1 NIH-BMAP_Ret4_S2 Mus musculus cDNA clone
mRNA sequence.
ACCESSION BE984614
VERSION BE984614.1 GI:10657016
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
TITLE Bonaldo.M.F., Lennon.G. and Soares.M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery

Query Match      0.9%; Score 23; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2627 gagtttgagaaaaa 2649
Db 25 GAGTTTTCAGAAAAA 3

RESULT 13
LOCUS B1283532/c 215 bp mRNA EST 19-JUL-2001
DEFINITION UI-R-CZ0-bzc-e-10-0-UI.s1 UI-R-CZ0 Rattus norvegicus cDNA clone
mRNA sequence.
ACCESSION B1283532
VERSION B1283532.1 GI:14935371
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
TITLE Rattus.
JOURNAL 1 (bases 1 to 215)
MEDLINE Bonaldo,M.F., Lennon,G. and Soares,M.B.
COMMENT Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized penis library cDNA Library preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..215
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CZ0-bzc-e-10-0-UI"
/clone_lib="UI-R-CZ0"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-CZ0
library is a non-normalized library constructed from rat
penis tissue. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratat.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG LIB=UI-R-CZ0
TAG-TISSUE=penis
TAG_SEQ=TTGCGGAACA"
BASE COUNT 43 a 55 c 54 g 63 t
ORIGIN

Query Match      0.9%; Score 23; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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